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OM nucleic - nucleic search, using sw model

Run on:

June 11, 2003, 17:57:02 ; Search time 2186 seconds

(without alignments)

10592.969 Million cell updates/sec

Title: US-09-308-397-1

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Listing first 45 summaries

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 25 344.4 37.4 942 31 US-09-815-242-6823
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 27 340.4 37.0 3656 14 US-09-070-927-577
 28 340.4 37.0 3656 14 US-09-070-927-577
 29 316.8 34.4 2969 49 US-09-070-927-577
 30 316.8 34.4 2969 50 US-09-068-186-533
 31 315.2 34.2 987 15 US-09-107-532-3319
 32 315.2 34.2 987 15 US-09-107-532-3319
 33 301 32.7 3627 48 US-09-046-649-929
 34 301 32.7 3627 48 US-09-046-649-929
 35 301 32.7 3627 50 US-09-058-217-903
 36 204 22.1 950 36 US-09-974-300-1086
 37 198.2 21.5 1002 21 US-09-543-681-2-3881
 39 196.4 21.3 939 31 US-09-815-242-6878
 40 196.4 21.3 939 31 US-09-815-242-6878
 41 196.4 21.3 939 39 US-09-070-851-6878
 C 42 196.4 21.3 1830121 8 US-08-426-7871
 C 43 196.4 21.3 1830121 22 US-09-557-884-1
 C 44 196.4 21.3 1830121 25 US-09-613-998A-1
 C 45 186.6 20.3 1198 27 US-09-680-598A-74
 Sequence 3, Appli
 Sequence 1582, Ap
 Sequence 6823, Ap
 Sequence 6823, Ap
 Sequence 6823, Ap
 Sequence 577, Ap
 Sequence 577, Ap
 Sequence 527, Ap
 Sequence 533, Ap
 Sequence 3319, Ap
 Sequence 3319, Ap
 Sequence 916, Ap
 Sequence 903, Ap
 Sequence 1143, Ap
 Sequence 1086, Ap
 Sequence 1811, Ap
 Sequence 6878, Ap
 Sequence 6878, Ap
 Sequence 1, Appli
 Sequence 1, Appli
 Sequence 74, Appli
 Qy 241 TATCAGCCTGATATGGCTTGGTCTTCGGAGATACTCTGCCTTGGTCCAAGC 300
 Db 241 TATCACCTGATATGGCTTGGTCTTCGGAGATACTCTGCCTTGGTCCAAGC 300
 Qy 301 GGCGCCCTGGATTGGAGATGGCCTTGGCTTAGCTAAGGCTGAGCTATAGGAA 360
 Db 301 GGCGCCCTGGATTGGAGATGGCCTTGGCTTAGCTAAGGCTGAGCTATAGGAA 360
 Qy 361 GAGGGGCTCTGTCAGTGGCAAGCTGAGCTGAGCTGAGCTGAGCTGAGGGC 420
 Db 361 GAGGGGCTCTGTCAGTGGCAAGCTGAGCTGAGCTGAGCTGAGCTGAGGGC 420
 Qy 421 ATTGAGAAGGCCTGCAAAAGCTGACTTGGAGTGGTTATCCACCAATAAAC 480
 Db 421 ATTGAGAAGGCCTGCAAAAGCTGACTTGGAGTGGTTATCCACCAATAAAC 480
 Qy 421 ATTGAGAAGGCCTGCAAAAGCTGACTTGGAGTGGTTATCCACCAACTATAAC 480
 Db 421 ATTGAGAAGGCCTGCAAAAGCTGACTTGGAGTGGTTATCCACCAACTATAAC 480
 Qy 481 ACACCTGCAAAATGTCATTGCTGAGAGTGGTGAACGGGTGAACT 540
 Db 481 ACACCTGCAAAATGTCATTGCTGAGAGTGGTGAACGGGTGAACT 540
 Qy 541 TTGCAAGAAGGGTGCACGCTTGTATGCCCTTAAGGTGAGTCCTTACACC 600
 Db 541 TTGCAAGAAGGGTGCACGCTTGTATGCCCTTAAGGTGAGTCCTTACACC 600
 Qy 601 GCTCTCTTGGTCAAGCTGCTAGCCGAACTAGCTGAAACTCTAGCTCAGTAAGTTTCA 660
 Db 601 GCTCTCTTGGTCAAGCTGCTAGCCGAACTAGCTGAAACTCTAGCTCAGTAAGTTTCA 660
 Qy 661 GATTTCATCTGTCCTGAGGCTTACAGGCTGATGCAAAAGGAGACATT 720
 Db 661 GATTTCATCTGTCCTGAGGCTTACAGGCTGATGCAAAAGGAGACATT 720
 Qy 721 GCTCACTCTGACCGCTTACGGTCAAGGACCCCTTCGTTCTAGAAAGTATGGGTC 780
 Db 721 GCTCACTCTGACCGCTTACGGTCAAGGACCCCTTCGTTCTAGAAAGTATGGGTC 780
 Qy 781 ATGCGAAGAAGGGATAAGCAACTTATCGAGTTGACCCGAAACTCTTCAGGT 840
 Db 781 ATGCGAAGAAGGGATAAGCAACTTATCGAGTTGACCCGAAACTCTTCAGGT 840
 Qy 841 TTGGTTAAAATGATAACCTGCTACTAGGTCAATGGGAGATAAGCCAGTTA 900
 Db 841 TTGGTTAAAATGATAACCTGCTACTAGGTCAATGGGAGATAAGCCAGTTA 900
 Qy 901 GTAGGACTTTAGAAAAATAG 921
 Db 901 GTAGGACTTTAGAAAAATAG 921

ALIGNMENTS

RESULT 1
 US-09-308-397-1
 Sequence 1, Application US/09308397
 GENERAL INFORMATION:
 APPLICANT: Gentry, Daniel R.
 APPLICANT: Lonsdale, John T.
 APPLICANT: Payne, David J.
 APPLICANT: Pearson, Stewart C.
 APPLICANT: Van Allen, Glenn
 TITLE OF INVENTION: Novel Fabb
 FILE REFERENCE: P50593
 CURRENT APPLICATION NUMBER: US/09/308,397
 CURRENT FILING DATE: 1999-05-18
 EARLIER APPLICATION NUMBER: US 60/031,160
 EARLIER FILING DATE: 1996-11-18
 EARLIER APPLICATION NUMBER: PCT/US97/20392
 EARLIER FILING DATE: 1997-11-14
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 921
 TYPE: DNA
 ORGANISM: Streptococcus pneumoniae
 US-09-308-397-1

Query Match 100.0%; Score 921; DB 17; Length 921;
 Best Local Similarity 100.0%; Pred. No. 2.1e-21;
 Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACTAAACAGCCTTATTGCTGTCAGTCAAGGCTGGAGGG 60
 Db 1 ATGACTAAACAGCCTTATTGCTGTCAGTCAAGGCTGGAGGG 60
 Qy 61 GATTTCATGATCAGTCCGATTCAGGAAACGATGATGAGGCTC 120
 Db 61 GATTTCATGATCAGTCCGATTCAGGAAACGATGATGAGGCTC 120
 Qy 121 CGTTATGATTACGTTATCTCATCGATACGAAACTCTAACATGAGGCTGGAGGG 180
 Db 121 CGTTATGATTACGTTATCTCATCGATACGAAACTCTAACATGAGGCTGGAGGG 180
 Qy 181 ACGCAACAGCATTCTGGAGACTCTGGTGTCTACCTGGTTATTCAGGAAAGGC 240
 Db 181 ACGCAACAGCATTCTGGAGACTCTGGTGTCTACCTGGTTATTCAGGAAAGGC 240

RESULT 2
 US-09-583-110-1251
 Sequence 1251, Application US/09583110
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 FILE REFERENCE: PAT1000A
 CURRENT APPLICATION NUMBER: US/09/583,110
 CURRENT FILING DATE: 2000-05-16
 PRIOR APPLICATION NUMBER: US 09/107,433
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: US 60/085,131
 PRIOR FILING DATE: 1998-05-12
 PRIOR APPLICATION NUMBER: US 60/051,553
 PRIOR FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 5322
 SEQ ID NO: 1251
 LENGTH: 921
 TYPE: DNA
 ORGANISM: Streptococcus pneumoniae
 US-09-583-110-1251

Query Match 99.1%: Score 913; DB 22; Length 921;
 Best Local Similarity 99.5%; Prd. No. 7e-269; Mismatches 5; Indels 0; Gaps 0;
 Matches 916; Conservative 0; Gaps 0;

Qy 1 ATGACTAAACAGCCTTTTATTGCGTCAGGTGCCAGTATCTAGGGATGGACGG 60
 Db 1 ATGACTAAACAGCCTTTTATTGCGTCAGGTGCCAGTATCTAGGGATGGACGG 60

Qy 61 GATTCTATGATCAGTAAACGATTGTCAAAGAAACGATGATCAGGGACTAGGTGCTC 120
 Db 61 GATTCTATGATCAGTAAACGATTGTCAAAGAAACGATGATCAGGGACTAGGTGCTC 120

Qy 121 GGTTATGATTAGTGTAACTCATGATAGTAAAGAAACAAACTCATAGACCCCTAT 180
 Db 121 GGTTATGATTGGTTAACTCATGATAGTAAAGAAACAAACTCATAGACCCCTAT 180

Qy 181 ACGAACAGCCATTCTGCACTTCGGTTGCTATCAACGTTTATTCAGAAAGGC 240
 Db 181 ACGAACAGCCATTCTGCACTTCGGTTGCTATCAACGTTTATTCAGAAAGGC 240

Qy 241 TATCAGCCTGATATGGTCTGTTGCTGTTGCTGTTGCTCTGGAAATACTCTGCCT 300
 Db 241 TATCAGCCTGATATGGTCTGTTGCTGTTGCTGTTGCTCTGGAAATACTCTGCCT 300

Qy 301 GGCCTCTGGATTGAGATGGCTCCCTTGAGTAAACGTGAGCCATATGGA 360
 Db 301 GGCCTCTGGATTGAGATGGCTCCCTTGAGTAAACGTGAGCCATATGGA 360

Qy 361 GAAAGGGCTCTGGTGAATCTGGCAAGATGGTAGCACTTCACAATAGCCAGTAGGTC 420
 Db 361 GAAAGGGCTCTGGTGAATCTGGCAAGATGGTAGCACTTCACAATAGCCAGTAGGTC 420

Qy 421 ATGAAAGAAGCCCTGTCAAAAGCTTCGAACCTGGAGTACTCCGCAACTATAAC 480
 Db 421 ATGAAAGAAGCCCTGTCAAAAGCTTCGAACCTGGAGTACTCCGCAACTATAAC 480

Qy 481 ACACCTGACAATCTGATTGCTGAACCTGGAGTACTCCGCAACTATAAC 540
 Db 481 ACACCTGACAATCTGATTGCTGAACCTGGAGTACTCCGCAACTATAAC 540

Qy 541 TTGAAAGAAGCAGTGCACAAACCGTTGATTCCTCTAAAGGTCTAGSTCCCTTCACCC 600
 Db 541 TTGAAAGAAGCAGTGCACAAACCGTTGATTCCTCTAAAGGTCTAGSTCCCTTCACCC 600

Qy 601 GCTCTCCCTGAGCTGCTAGCCAGAAACTCTAGTGAAGTTTCA 660
 Db 601 GCTCTCCCTGAGCTGCTAGCCAGAAACTCTAGTGAAGTTTCA 660

Qy 661 GATTTTATCTGTCCTCCPAGTCGGCAATTAGCAAGAGCTGCTGTTGATGAAAGGACATT 720
 Db 661 GATTTTATCTGTCCTCCPAGTCGGCAATTAGCAAGAGCTGCTGTTGATGAAAGGACATT 720

Qy 721 GCTCAGCTCTGAGCGCTAGGTCAAGGAACCCGTTCTATGAAGAATGGGTCT 780
 Db 721 GCTCAGCTCTGAGCGCTAGGTCAAGGAACCCGTTCTATGAAGAATGGGTCT 780

Qy 781 ATGAAAGAAGCAGCACTAGCAACTTCTGAGATTGACCGGGAAAGTCCTGTAAGT 840
 Db 781 ATGAAAGAAGCAGCACTAGCAACTTCTGAGATTGACCGGGAAAGTCCTGTAAGT 840

Qy 841 TTGTTAAAAATGATCCTGTCACCTAGCTGAAAGATCAAGCGAGTTA 900
 Db 841 TTGTTAAAAATGATCCTGTCACCTAGCTGAAAGATCAAGCGAGTTA 900

Qy 901 GTAGGACTTTGAAATAAG 921
 Db 901 GTAGGACTTTGAAATAAG 921

RESULT 3
 US-09-308-30
 Sequence 30: Application US/09752069A
 GENERAL INFORMATION:

APPLICANT: Dougherty, Thomas J.
 APPLICANT: Pucci, Michael J.
 APPLICANT: Dougherty, Brian A.
 APPLICANT: Davison, Daniel B.
 APPLICANT: Brucoceleri, Robert E.
 APPLICANT: Thanassi, Jane A.
 APPLICANT: Farmer II, Bennett T.
 TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
 FOR CELL VIABILITY AND THEIR USES
 FILE REFERENCE: D001NP
 CURRENT APPLICATION NUMBER: US/09/752,069A
 CURRENT FILING DATE: 2000-12-29
 PRIORITY APPLICATION NUMBER: 60/174,089
 PRIORITY FILING DATE: 1999-12-30
 NUMBER OF SEQ ID NOS: 338
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 30
 LENGTH: 921
 TYPE: DNA
 ORGANISM: *Streptococcus pneumoniae*
 US-09-752,069A-30

Query Match 99.1%; Score 913; DB 29; Length 921;
 Best Local Similarity 99.5%; Pred. No. 7e-269; Length 921;
 Matches 916; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGACTAAACAGCCTTTTATTGCGTCAGGTGCCAGTATCTAGGGATGGACGG 60
 Db 1 ATGACTAAACAGCCTTTTATTGCGTCAGGTGCCAGTATCTAGGGATGGACGG 60

Qy 121 GGTTATGATTAGTGTAACTCATGATAGTAAAGAAACAAACTCATAGACCCCTAT 180
 Db 121 GGTTATGATTGGTTAACTCATGATAGTAAAGAAACAAACTCATAGACCCCTAT 180

Qy 181 ACGAACAGCCATTCTGCACTTCGGTTGCTATCAACGTTTATTCAGAAAGGC 240
 Db 181 ACGAACAGCCATTCTGCACTTCGGTTGCTATCAACGTTTATTCAGAAAGGC 240

Qy 241 TATCAGCCTGATATGGTCTGTTGCTGTTGCTCTGGAAATACTCTGCCT 300
 Db 241 TATCAGCCTGATATGGTCTGTTGCTGTTGCTCTGGAAATACTCTGCCT 300

Qy 301 GGCCTCTGGATTGAGATGGCTCCCTTGAGTAAACGTGAGCCATATGGA 360
 Db 301 GGCCTCTGGATTGAGATGGCTCCCTTGAGTAAACGTGAGCCATATGGA 360

Qy 361 GAAAGGGCTCTGGTGAATCTGGCAAGATGGTAGCACTTCACAATAGCCAGTAGGTC 420
 Db 361 GAAAGGGCTCTGGTGAATCTGGCAAGATGGTAGCACTTCACAATAGCCAGTAGGTC 420

Qy 421 ATGAAAGAAGCCCTGTCAAAAGCTTCGAACCTGGAGTACTCCGCAACTATAAC 480
 Db 421 ATGAAAGAAGCCCTGTCAAAAGCTTCGAACCTGGAGTACTCCGCAACTATAAC 480

Qy 481 ACACCTGACAATCTGATTGCTGAACCTGGAGTACTCCGCAACTATAAC 540
 Db 481 ACACCTGACAATCTGATTGCTGAACCTGGAGTACTCCGCAACTATAAC 540

Qy 541 TTGAAAGAAGCAGTGCACAAACCGTTGATTCCTCTAAAGGTCTAGSTCCCTTCACCC 600
 Db 541 TTGAAAGAAGCAGTGCACAAACCGTTGATTCCTCTAAAGGTCTAGSTCCCTTCACCC 600

Qy 601 GCTCTCCCTGAGCTGCTAGCCAGAAACTCTAGTGAAGTTTCA 660
 Db 601 GCTCTCCCTGAGCTGCTAGCCAGAAACTCTAGTGAAGTTTCA 660

Qy 661 GATTTTATCTGTCCTCCPAGTCGGCAATTAGCAAGAGCTGCTGTTGATGAAAGGACATT 720
 Db 661 GATTTTATCTGTCCTCCPAGTCGGCAATTAGCAAGAGCTGCTGTTGATGAAAGGACATT 720

Qy 721 GCTCAGCTCTGAGCGCTAGGTCAAGGAACCCGTTCTATGAAGAATGGGTCT 780
 Db 721 GCTCAGCTCTGAGCGCTAGGTCAAGGAACCCGTTCTATGAAGAATGGGTCT 780

Qy 781 ATGAAAGAAGCAGCACTAGCAACTTCTGAGATTGACCGGGAAAGTCCTGTAAGT 840
 Db 781 ATGAAAGAAGCAGCACTAGCAACTTCTGAGATTGACCGGGAAAGTCCTGTAAGT 840

Qy 841 TTGTTAAAAATGATCCTGTCACCTAGCTGAAAGATCAAGCGAGTTA 900
 Db 841 TTGTTAAAAATGATCCTGTCACCTAGCTGAAAGATCAAGCGAGTTA 900

Qy 901 GTAGGACTTTGAAATAAG 921
 Db 901 GTAGGACTTTGAAATAAG 921

Query Match 99.1%; Score 913; DB 29; Length 921;
 Best Local Similarity 99.5%; Pred. No. 7e-269; Length 921;
 Matches 916; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGACTAAACAGCCTTTTATTGCGTCAGGTGCCAGTATCTAGGGATGGACGG 60
 Db 1 ATGACTAAACAGCCTTTTATTGCGTCAGGTGCCAGTATCTAGGGATGGACGG 60

Qy 121 GGTTATGATTAGTGTAACTCATGATAGTAAAGAAACAAACTCATAGACCCCTAT 180
 Db 121 GGTTATGATTGGTTAACTCATGATAGTAAAGAAACAAACTCATAGACCCCTAT 180

Qy 181 ACGAACAGCCATTCTGCACTTCGGTTGCTATCAACGTTTATTCAGAAAGGC 240
 Db 181 ACGAACAGCCATTCTGCACTTCGGTTGCTATCAACGTTTATTCAGAAAGGC 240

Qy 241 TATCAGCCTGATATGGTCTGTTGCTGTTGCTCTGGAAATACTCTGCCT 300
 Db 241 TATCAGCCTGATATGGTCTGTTGCTGTTGCTCTGGAAATACTCTGCCT 300

Qy 301 GGCCTCTGGATTGAGATGGCTCCCTTGAGTAAACGTGAGCCATATGGA 360
 Db 301 GGCCTCTGGATTGAGATGGCTCCCTTGAGTAAACGTGAGCCATATGGA 360

Qy 361 GATTTTATCTGTCCTCCPAGTCGGCAATTAGCAAGAGCTGCTGTTGATGAAAGGACATT 420
 Db 361 GATTTTATCTGTCCTCCPAGTCGGCAATTAGCAAGAGCTGCTGTTGATGAAAGGACATT 420

Qy 421 ATGAAAGAAGCCTGTCAAAAGCTGCTAGCTGAGTAACTCTAGCTGAAACTATAAC 480
 Db 421 ATGAAAGAAGCCTGTCAAAAGCTGCTAGCTGAGTAACTCTAGCTGAAACTATAAC 480

Qy 481 ACACCTGACAATCTGATTGCTGAACCTGGAGTACTCCGCAACTCTAGCTGAAACTATAAC 540
 Db 481 ACACCTGACAATCTGATTGCTGAACCTGGAGTACTCCGCAACTCTAGCTGAAACTATAAC 540

Qy 541 TTGCTCCCTGAGCTGCTAGCCAGAAACTCTAGCTGAAACTCTAGCTGAAACTATAAC 600
 Db 541 TTGCTCCCTGAGCTGCTAGCCAGAAACTCTAGCTGAAACTCTAGCTGAAACTATAAC 600

Qy 601 GCTCTCCCTGAGCTGCTAGCCAGAAACTCTAGCTGAAACTCTAGCTGAAACTATAAC 660
 Db 601 GCTCTCCCTGAGCTGCTAGCCAGAAACTCTAGCTGAAACTCTAGCTGAAACTATAAC 660

Qy 661 GATTTTACTGTCCTCTAGGAAATAAGCTGCTGTTGATGAAAGCTGCTGTTGATGAAAGGACATT 720
 Db 661 GATTTTACTGTCCTCTAGGAAATAAGCTGCTGTTGATGAAAGCTGCTGTTGATGAAAGGACATT 720

QY 721 GCTCAGGCTCTGACGGTCAGGCAAGGAAACCGTTCTATGAANGTATGGGTC 780
 .Db 721 GCTCAGGCTCTGACGGTCAGGCAAGGAAACCGTTCTATGAANGTATGGGTC 780

QY 781 ATGCAAGAAGGGCATAGAAACTTATGAGATTGGCAGGGAAAGTCCTGTCAGT 840
 .Db 781 ATGCAAGAAGGGCATAGAAACTTATGAGATTGGCAGGGAAAGTCCTGTCAGT 840

QY 841 TTGTTAAAAATCATCAAACTGCTCAATTAGTCATGGAGATAAGCCAGTTA 900
 .Db 841 TTGTTAAAAATCATCAAACTGCTCAATTAGTCATGGAGATAAGCCAGTTA 900

QY 901 GTAGGACTTTAGAAGAATAG 921
 .Db 901 GTAGGACTTTAGAAGAATAG 921

RESULT 4
 US-60-174-089-30
 / Sequence, Application US/60174089
 / GENERAL INFORMATION:
 / APPLICANT: Dougherty, Thomas J.
 / APPLICANT: Pucci, Michael J.
 / APPLICANT: Dougherty, Brian A.
 / INVENTION: Davidson, Daniel B.
 / TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
 / FILE REFERENCE: 30436 44USP1
 / CURRENT APPLICATION NUMBER: US/60/174,089
 / CURRENT FILING DATE: 1999-12-30
 / NUMBER OF SEQ ID NOS: 226
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 30
 / LENGTH: 921
 / TYPE: DNA
 / ORGANISM: Streptococcus pneumoniae
 US-60-174-089-30

Query Match 99.1%; Score 913; DB 61; Length 921;
 Best Local Similarity 99.5%; Pred. No. 7e-269;
 Matches 916; Conservative 0; N mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACTAAAGCCATTATTGCTGTCAGGTCAGATCTAGGATGGGAGGG 60
 .Db 1 ATGACTAAAGCCATTATTGCTGTCAGGTCAGATCTAGGATGGGAGGG 60

QY 61 GATTCTATGATGATGATCCATTGTCAGATGGTAAAGAACGATGATGGTC 120
 .Db 61 GATTCTATGATGATGATCCATTGTCAGATGGTAAAGAACGATGATGGTC 120

QY 121 GTTATAATTAGTTATCTCATGATGATGTCAGGAAACCTAACTGATGGTC 180
 .Db 121 GTTATAATTAGTTATCTCATGATGATGTCAGGAAACCTAACTGATGGTC 180

QY 181 AGCCACAGCCATTAGGCACTTGGCTGCTATCACCGTTATGGAAAGGGC 240
 .Db 181 AGCCACAGCCATTAGGCACTTGGCTGCTATCACCGTTATGGAAAGGGC 240

QY 241 TATCAGCTGTATGTTGCTGCTCTGGAAATACTCTGCTGGCAAGGC 300
 .Db 241 TATCAGCTGTATGTTGCTGCTCTGGAAATACTCTGCTGGCAAGGC 300

QY 301 GGCCTTGGATTTCAGAATGGCTGGCTAGGCTTAAGCTGGCCCTATGGAA 360
 .Db 301 GGCCTTGGATTTCAGAATGGCTGGCTAGGCTTAAGCTGGCCCTATGGAA 360

QY 361 GAGGCGCTCTGGCTGTAAGCTGGCAAGTGGCTCAATGCCAGTAGGTC 420
 .Db 361 GAGGCGCTCTGGCTGTAAGCTGGCAAGTGGCTCAATGCCAGTAGGTC 420

QY 421 ATTGAGAAGCTGTSAAAAAGCTCTGACTTGGAGTTACTCCAGCCAACTATAAC 480

Db 421 ATTGAGAAGCTGTSAAAAAGCTCTGACTTGGAGTTACTCCAGCCAACTATAAC 480

QY 481 ACACCTGCACAAATCGTCATGTCAGAAGTGGCTGACTTGATGAGGGTTAACCT 540
 .Db 481 ACACCTGCACAAATCGTCATGTCAGAAGTGGCTGACTTGATGAGGGTTAACCT 540

QY 541 TTGCAAGAAGGGTGCACAAAGCTGTAAGTGTCTCTTAAGGTGTCGGTCCCTTACACC 600
 .Db 541 TTGCAAGAAGGGTGCACAAAGCTGTAAGTGTCTCTTAAGGTGTCGGTCCCTTACACC 600

QY 601 GCTCTCTTGCCTGCTAGCCACTAGCAGAACTCTAGCTAGTAAGTTTCA 660
 .Db 601 GCTCTCTTGCCTGCTAGCCACTAGCAGAACTCTAGCTAGTAAGTTTCA 660

QY 661 GATTTTACTTGTGCCCTAGTGGCAATACAAGACCTGCTGTCATAAAAGGACATT 720
 .Db 661 GATTTTACTTGTGCCCTAGTGGCAATACAAGACCTGCTGTCATAAAAGGACATT 720

QY 721 GCTCTCTTGCCTGCTAGCCACTAGCAGAACTCTAGCTAGTAAGTTTCA 780
 .Db 721 GCTCTCTTGCCTGCTAGCCACTAGCAGAACTCTAGCTAGTAAGTTTCA 780

QY 781 ATGCGAAGGAGGCCATAAGCAACCTTATCGATGGACGGGAAAGCTGTCAGGT 840
 .Db 781 ATGCGAAGGAGGCCATAAGCAACCTTATCGATGGACGGGAAAGCTGTCAGGT 840

QY 841 TTGTTAAAAATGATCATACAGTCACTAGTCATGTGAGATCAAGCGTTTA 900
 .Db 841 TTGTTAAAAATGATCATACAGTCACTAGTCATGTGAGATCAAGCGTTTA 900

QY 901 GTAGCATTTTAGAAGAATAG 921
 .Db 901 GTAGCATTTTAGAAGAATAG 921

RESULT 5
 US-09-174-089-30
 / Sequence 794, Application US/09107433
 / GENERAL INFORMATION:
 / APPLICANT: Lynn A. Doucette-Stamm and David Bush
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
 / SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
 / FOR DIAGN

NUMBER OF SEQUENCES: 5206
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 / STREET: 100 Beaver Street
 / CITY: Waltham
 / STATE: Massachusetts
 / ZIP: 02454
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: CD-ROM ISO9660
 / COMPUTER: <Unknown>
 / OPERATING SYSTEM: <Unknown>
 / SOFTWARE: <Unknown>
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: 60/085131
 / FILING DATE: May 12, 1998
 / APPLICATION NUMBER: 60/081553
 / FILING DATE: July 2, 1997
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Arinello, Pamela Deneke
 / REGISTRATION NUMBER: 40-489
 / REFERENCE/DOCKET NUMBER: GTC-011
 / TELECOMMUNICATION INFORMATION
 / TELEPHONE: (781)893-5007
 / TELEFAX: (781)893-8277
 / INFORMATION FOR SEQ ID NO: 794:
 / SEQUENCE CHARACTERISTICS:

LENGTH: 924 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Streptococcus pneumoniae
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1...924
 SEQUENCE DESCRIPTION: SEQ ID NO: 794:
 US-09-10743-794

RESULT 6
 US-10-158-844-7/c
 Sequence 7, Application US/10158844
 ; GENERAL INFORMATION:
 ; APPLICANT: Kunsch et al.
 ; NUMBER OF SEQUENCES: 391
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-R
 ; COMPUTER: Dell Latitude Pentium 3
 ; OPERATING SYSTEM: Windows 98
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/158 844
 ; FILING DATE: 03-Jun-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/961,527
 ; FILING DATE: 1997-10-30
 ; APPLICATION NUMBER: US 60/029,960
 ; FILING DATE: 1996-10-31
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hyman, Mark J.
 ; REGISTRATION NUMBER: 46,789
 ; REFERENCE/DOCKET NUMBER: FB340P1D1
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19702 base pairs
 ; TYPE: nucleic acid
 ; STRANDDNESS: double
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-158-844-7

Query Match 99.1%; Score 913; DB 15; Length 924;
 Best Local Similarity 99.5%; Pred. No. 7e-269; 5; Indels 0; Gaps 0;
 Matches 916; Conservative 0; Mismatches 5; Gaps 0;

Db 1 ATGACTAAACAGCCTTTATTCTGGTCAAGGTGGCTACTAGGGATGGGACGG 60
 Db 4 ATGACTAAACAGCCTTTATTCTGGTCAAGGTGGCTACTAGGGATGGGACGG 63

Qy 61 GATTCTTATGATCAGTATCGATGTCAGGAAAGATGATCGAGCGATCGGGTC 120
 Db 64 GATTCTTATGATCAGTATCGATGTCAGGAAAGATGATCGAGCGATCGGGTC 123

Qy 121 GTTATGATTACGTATTCATCGATCCATCGAAACTCAATGACCGCTAT 180
 Db 124 GTTATGATTACGTATTCATCGATCCATCGAAACTCAATGACCGCTAT 183

Qy 181 ACGAACAGCAGCATCTAGGACACTGGTGTCTACCGTTATGGAAAGGC 240
 Db 184 ACGAACAGCAGCATCTAGGACACTGGTGTCTACCGTTATGGAAAGGC 243

Qy 241 TATCAGCTGATGATGTTGCTGGTCTTGGAACTCTGGCTGGCAAGC 300
 Db 244 TATCAGCTGATGATGTTGCTGGTCTTGGAACTCTGGCTGGCAAGC 303

Qy 301 GGCGCCTGGATTGAAAGATGCGGTTGGCTTAGCTAAGGTGGACCTATATGAA 360
 Db 304 GGCGCTTGGATTGAAAGATGCGGTTGGCTTAGCTAAGGTGGACCTATATGAA 363

Qy 361 GAAAGGGCTCTGCTGACTCTGGCAGAATGGTAGCTCAATACGCCAGTAGAGTC 420
 Db 364 GAAAGGGCTCTGCTGACTCTGGCAGAATGGTAGCTCAATACGCCAGTAGAGTC 423

Qy 421 ATTGAAAGAGCTGTCANAAAGCTGTGACTCTGAACTTAACTCCAGCCAACTATAAC 480
 Db 424 ATTGAAAGAGCTGTCANAAAGCTGTGACTCTGAACTTAACTCCAGCCAACTATAAC 483

Qy 481 ACACCTGACAATGTCATGTCAGTGGAGGTGGCTGATGACGGTTGAAT 540
 Db 484 ACACCTGACAATGTCATGTCAGTGGAGGTGGCTGATGACGGTTGAAT 543

Qy 541 TTGCAAGGAGGAGGTCACGCTTCAACGCTTCAAGCTGTCAGGTTTCACAC 600
 Db 544 TTGCAAGGAGGAGGTCACGCTTCAACGCTTCAAGCTGTCAGGTTTCACAC 603

Qy 601 GCTCTCTGAGCCCTGCTAGCAGAAACTAGCTGAAACTCTAGCTAAGTTTCAC 660
 Db 604 GCTCTCTGAGCCCTGCTAGCAGAAACTAGCTGAAACTCTAGCTAAGTTTCAC 663

Db 661 GATTTCATCTCCCTAATGGCAAAATAGAAAGCTGCTGTGATGCAAAGAGGACAT 720
 Qy 664 GATTTCATCTCCCTAATGGCAAAATAGAAAGCTGCTGTGATGCAAAGAGGACAT 723

Db 721 GCTCACTCTGACGGTCAAGTCAGGAACTAGCTGAAACTCTAGCTAAGTTTCAC 780
 Db 724 GCTCACTCTGACGGTCAAGTCAGGAACTAGCTGCTGTGATGCAAATGGCTC 783

Qy 781 ATGCAAGAGGAGGATAAGCAACTTATGAGATTGGACGGGAAAGTCGTCAAGT 840

Db 784 ATGCAAGAGGAGGATAAGCAACTTATGAGATTGGACGGGAAAGTCGTCAAGT 843

Qy 841 TTGTTAAATGATCAGTAAACTGTCAGTCTAGCTCATGTCAGGAACTCAAGCGACTTA 900
 Db 844 TTGTTAAATGATCAGTAAACTGTCAGTCTAGCTCATGTCAGGAACTCAAGCGACTTA 903

Qy 901 GTAGCACTTTAGAAATAG 921
 Db 904 GTAGCACTTTAGAAATAG 924

Qy 1 ATGCTTATGATCAGTATCGATGTCAGGAAAGATGATCGAGCGATCGGGTC 120
 Db 17089 GATTCTTATGATCAGTATCGATGTCAGGAAAGATGATCGAGCGATCGGGTC 17090
 Qy 121 GTTATGATTACGTATTCATCGATCCATCGAAACTCAATGACCGCTAT 180
 Db 17149 ATGACTAAACAGCCTTTATTCTGGCTGGACCTAT 181
 Qy 61 GATTCTTATGATCAGTATCGATGTCAGGAAAGATGATCGAGCGATCGGGTC 120
 Db 17170 GATTCTTATGATCAGTATCGATGTCAGGAAAGATGATCGAGCGATCGGGTC 17170
 Qy 181 AGGCAACAGCAGCATCTAGGACACTGGTGTCTACCGTTATGGCAAGAAAGGC 240
 Db 16569 AGGCAACAGCAGCATCTAGGACACTGGTGTCTACCGTTATGGCAAGAAAGGC 16510
 Qy 241 TATCAGCTGATGATGTTGCTGGTCTTGGCTGAAATACTGCTTGGCAAGC 300

FILING DATE: / / / / / /

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE DOCKET NUMBER: PB340PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 19706 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-60-029-960-61

Query Match 99.1%; Score 913; DB 46; Length 19706;
Best Local Similarity 99.5%; Pred. No. 2,9e-28;
Matches 916; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGACTAAACGCCCCCTTATTCTGGTCAAGGGCCAGTATCTAGGGATGGACGG 60
Db 17155 ATGACTAAACGCCCCCTTATTCTGGTCAAGGGCCAGTATCTAGGGATGGACGG 1709

Qy 61 GATTCTATGATAGTATCCGATTGCAAGAAACGATTGATGAGGCCAGTCAAGGTGTC 120
Db 17095 GATTCTATGATGATTCGATTCGATTGTAAGAAACGATTGATGAGGCCAGTCAAGGTGTC 1703

Qy 121 CGTTATGATTAGTATAGTATCTATGATACTGAGAAAGCATAACTCAATCAGACCGCTAT 180
Db 17035 GTTATGATTAGTATCTATGATACTGAGAAAGCATAACTCAATCAGACCGCTAT 1697

Qy 601 GCTCTCTTGGCTGCTGAGCTGAGCTGAGCTGAGCTGAAACTCTAGCTCAGGAAGTTTC 660
Db 16549 GCTCTCTTGAACCTGTAACCTGTAACCTGAAACTAGCTGAAACTAGCTCAGGAAGTTTC 16490

Qy 661 GATTTAATCTGTCCTCTAGTGCSCAATACAGAAGCTGTTGATGCAAAAGGAGCAT 720
Db 16489 GATTTAATCTGTCCTCTAGTGCSCAATACAGAAGCTGTTGATGCAAAAGGAGCAT 16430

Qy 721 GCTCAGCTCTGAGCGGTAGGGTCAAGGAACCCGGTCTCTTCTATGAAAGTATGGGT 780
Db 16429 GCTCAGCTCTGAGCGGTAGGGTCAAGGAACCCGGTAACTGGTCAAGGAAGCTT 16370

Qy 781 ATGCAAGAAGCAGGCAATAGCAACTTATCGAATTGCAAGGGAAAGCTTGTCTAGGT 840
Db 16369 ATGCAAGAAGCAGGCAATAGCAACTTATCGAATTGCAAGGGAAAGCTTGTCTAGGT 16310

Qy 841 TTGTTAAAAAATTGATCAAACCTGCTCACTAGCTCATGTTGAAGATCAAGCGAGTTA 900
Db 16309 TTGTTAAAAAATTGATCAAACCTGCTCACTAGCTCATGTTGAAGATCAAGCGAGTTA 16250

Qy 901 GTAGCACTTTAGAAAAATAG 921
Db 16249 GTAGCACTTTAGAAAAATAG 16229

RESULT 7
US-60-029-960-61/c
Sequence 61. Application US/60029960
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 1649
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/133
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/029, 960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 781 ATGCAAGAAGCAGGCAATAGCAACTTATCGAAGATGGACGGAAAGCTGTCAAGTTTCA 840

RESULT 8
 PCT-US02-03987-9482
 / GENERAL INFORMATION:
 / APPLICANT: Elipta Pharmaceuticals, Inc.
 / TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
 / FILE REFERENCE: ELIPTA.C028VPC
 / CURRENT FILING DATE: 2002-02-02
 / PRIOR APPLICATION NUMBER: 60/267,636
 / PRIOR FILING DATE: 2001-02-09
 / NUMBER OF SEQ ID NOS: 15811
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 9182
 / LENGTH: 921
 / TYPE: DNA
 / ORGANISM: Streptococcus pneumoniae
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1) ... (921)

Query Match 99 0%: Score 911.4; DB 1; Length 921;
 Best Local Similarity 99.3%; Pred. No. 2.2e-268; Indels 0; Gaps 0;
 Matches 915; Conservative 0; Mismatches 6;

Db 1 ATGACTAAACAGCCCTTATTCATTCTGTCAAAGTGCCTACGGATGGATGGACGC 60
 Db 1 ATGACTAAACAGCCCTTATTCATTCTGTCAAAGTGCCTACGGATGGATGGACGC 60
 Db 1 GATTCTAATGCACTATCGATGTCATGCAAGAAACGATGATCAAGCACTTACG 120
 Db 61 GATTCTAATGCACTATCGATGTCATGCAAGAAACGATGATCAAGCACTTACG 120
 Db 121 GGTTATGATTTACGTTATCTCATGATAAGAACCTCAATAGACCCGATA 180
 Db 121 GGTTATGATTTACGTTATCTCATGATAAGAACCTCAATAGACCCGATA 180
 Qy 181 AGCDAACCAGCCATCTAGGACTCTGGCTGCTATCTACCGTTATGCCAAGAAACGC 240
 Db 181 AGCDAACCAGCCATCTGGACTCTGGCTGCTATCTACCGTTATGCCAAGAAACGC 240
 Qy 241 TATCAGCCCTGATATGGTGTGGTTCTCTGGAGAATACTCTGGCTTGGGGCAAGC 300
 Db 241 TATCAGCCCTGATATGGTGTGGCTTGGGGCAAGC 300
 Qy 361 GAAGGGGTCTGTGACTCTGGCAAGAATGGTACAGTCTCATACCCAGTAGAGTC 420
 Db 361 GAAGGGGTCTGTGACTCTGGCAAGAATGGTACAGTCTCATACCCAGTAGAGTC 420
 Pb 301 GGCGCTTGTGATTGAAATGGCTGCTTGTGCTTAGCTAGCTGGCTGGCCCTATGAA 360
 Db 301 GGCGCTTGTGATTGAAATGGCTGCTTGTGCTTAGCTAGCTGGCTGGCCCTATGAA 360
 Qy 421 ATTGAAAGGCTGTCAAAAGCTCTGAACTTGTGACTTGTGAGCTTACTCCAGCAACTATAAC 480
 Db 421 ATTGAAAGGCTGTCAAAAGCTCTGAACTTGTGACTTGTGAGCTTACTCCAGCAACTATAAC 480
 Qy 481 ACACCTGACAAATGTCAATGCTGACTCTGGAAAGTGGTGTGAGGGTGAACCT 540
 Db 541 TTGCAAGAAGGAGGTCACCAAAACGCTTGTGATTCCTCTTAAGGTGTCAGTCCTTCATACACC 600
 Db 541 TTGCAAGAAGGAGGTCACCAAACTGTTGATTCCTCTTAAGGTGTCAGTCCTTCATACACC 600
 Qy 601 GCTCTCTTGTGACCTGCTAGCAGAACTAGCTGAACACTAGCTGAAGTGTTCAT 660
 Db 601 GCTCTCTTGTGACCTGCTAGCAGAACTAGCTGAACACTAGCTGAAGTGTTCAT 660
 Qy 661 GATTACTCTCCCTAGTGGCATACAGAAGTGTGCTTCTATGAAAGTGGGACATT 720
 Db 661 GATTACTCTCCCTAGTGGCATACAGAAGTGTGCTTCTATGAAAGTGGGACATT 720
 Qy 721 GCTCAGCTCTGACGGCTCAGTCAGGACCCGTTGCTGTTCTATGAAAGTGGGTC 780
 Db 721 GTCAGCTCTGACGGCTCAGTCAGGAACTGGTCTTCTAGAAAGTGGGTC 780
 Qy 781 ATGCAAGAAGCAGGCTAAAGAACCTATCGAGATGGACCTGGAAAGTGTGTCAGGT 840
 Db 781 ATGCAAGAAGCAGGCTAAAGAACCTATCGAGATGGACCTGGAAAGTGTGTCAGGT 840
 Qy 841 TTGTTAAAAAAATGATCAAAACTGTCACUTAGCTCATGGAAAGTGTGTCAGGT 900
 Db 841 TTGTTAAAAAAATGATCGACTGTCACUTAGCTCATGGAAAGTGTGTCAGGT 900
 Qy 901 GTAGGACTTTAGAAATAG 921
 Db 901 GTAGGACTTTAGAAATAG 921

RESULT 9
 US-09-815-242-9482
 / Sequence 9482, Application US/09B15242
 / GENERAL INFORMATION:
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Ohlsen, Kari L.
 / APPLICANT: Zyskind, Judith W.
 / APPLICANT: Wall, Daniel
 / APPLICANT: Trawick, John D.
 / APPLICANT: Carr, Grant J.
 / APPLICANT: Yamamoto, Robert T.
 / APPLICANT: Xu, H. Howard
 / TITLE OF INVENTION: Identification of Essential Genes in
 / TITLE OF INVENTION: Prokaryotes
 / FILE REFERENCE: EULTRA.011A
 / CURRENT APPLICATION NUMBER: US/09/815,242
 / PRIOR APPLICATION NUMBER: 60/191,078
 / PRIOR FILING DATE: 2000-03-21
 / PRIOR APPLICATION NUMBER: 60/206,848
 / PRIOR FILING DATE: 2000-05-23
 / PRIOR APPLICATION NUMBER: 60/207,727
 / PRIOR FILING DATE: 2000-05-26
 / PRIOR APPLICATION NUMBER: 60/242,578
 / PRIOR FILING DATE: 2000-10-23
 / PRIOR APPLICATION NUMBER: 60/253,625
 / PRIOR FILING DATE: 2000-11-27
 / PRIOR FILING DATE: 2000-12-22
 / PRIOR APPLICATION NUMBER: 60/269,308
 / PRIOR FILING DATE: 2001-02-16
 / NUMBER OF SEQ ID NOS: 14110
 / SOFTWARE: FactsBQ for Windows Version 4.0
 / SEQ ID NO: 9482
 / LENGTH: 921
 / TYPE: DNA
 / ORGANISM: Streptococcus pneumoniae
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1) ... (921)
 US-09-815-242-9482

Query Match Score 911.4; DB 31; Length 921;
 Best Local Similarity 99.3%; Pred. No. 2.2e-268;
 Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGACTAAACAGCCTTTTATTGCTCTCAAGGTGCCAATCTTGGATGGACGG 60
 Db 1 ATGACTAAACAGCCTTTTATTGCTCTCAAGGTGCCAATCTTGGATGGACGG 60
 Qy 61 GATTCTATGATCAGTATTCGATGTCAGAACAGATGATCAGGGAGTCAGGGCTC 120
 Db 61 GATTCTATGATCAGTATTCGATGTCAGAACAGATGATCAGGGAGTCAGGGCTC 120
 Qy 121 GGTTATGTTACCTTATCTCATGATCAGAACAGCAACTCTCATAGACCCGAT 180
 Db 121 GGTTATGTTGCCTTATCTCATGATCAGAACAGCAACTCTCATAGACCCGAT 180
 Qy 181 ACGAACACGCCATTCTACGACTCTGGTTGATCAGCTTATTGCAAGAAAGGGC 240
 Db 181 ACGAACACGCCATTCTACGACTCTGGTTGATCAGCTTATTGCAAGAAAGGGC 240
 Qy 241 TATAGCCTGATATGGTCTGGTTGCTGGAAACCTTATGGAA 300
 Db 241 TATAGCCTGATATGGTCTGGTTGCTGGAAACCTTATGGAA 300
 Qy 301 GGCCCTTGATTGATGAGATGGCTTCCCTTGATGGCTTAAGGCTTATGGAA 360
 Db 301 GGCCCTTGATTGATGAGATGGCTTCCCTTGATGGCTTAAGGCTTATGGAA 360
 Qy 361 GAAACGGCTTCCTGTGATCTGCAAGTGGTAACTCCAGTAACTAC 420
 Db 361 GAAACGGCTTCCTGTGATCTGCAAGTGGTAACTCCAGTAACTAC 420
 Qy 421 ATTGAAAGAAAGCCTGTCAAAAGCTTCTGAACTTGGTTTACTCCAGCAACTATAC 480
 Db 421 ATTGAAAGAAAGCCTGTCAAAAGCTTCTGAACTTGGTTTACTCCAGCAACTATAC 480
 Qy 481 ACACCTGACAAATCTGATTGTGGAAAGGGTGAAGTGTATCGCGTTGAACCT 540
 Db 481 ACACCTGACAAATCTGATTGTGGAAAGGGTGAAGTGTATCGCGTTGAACCT 540
 Qy 541 TTGAAGAAGCAGTGCACAACTCCCTTCAACCC 600
 Db 541 TTGAAGAAGCAGTGCACAACTCCCTTCAACCC 600
 Qy 601 GCTCTCCCTGAGCCTGCTAGCCAAAGAAACTAGCTGAAACTCTAGCTGAAAGTTTCA 660
 Db 601 GCTCTCCCTGAGCCTGCTAGCCAAAGAAACTAGCTGAAACTCTAGCTGAAAGTTTCA 660
 Qy 661 GATTTTACCTTGTGCTCTAGTCGCAAAATCAGAAAGCTGTGTGATGAAAGGAGGATT 720
 Db 661 GATTTTACCTTGTGCTCTAGTCGCAAAATCAGAAAGCTGTGTGATGAAAGGAGGATT 720
 Qy 721 GCTCAGCCCTTGAGCCCTGAGCTCAAGGAAACCGCTTCTATGAAAGTATGGCT 780
 Db 721 GCTCAGCCCTTGAGCCCTGAGCTCAAGGAAACCGCTTCTATGAAAGTATGGCT 780
 Qy 781 ATGGAAGAAGCAGCATAGCAACTTATCTGAGATTGACCCGGAAAGTCTTGTCAAGT 840
 Db 781 ATGGAAGAAGCAGCATAGCAACTTATCTGAGATTGACCCGGAAAGTCTTGTCAAGT 840
 Qy 841 TTGTAAAAAATTGATCAAATCTGCTAAGTGTGAAAGATCAGCGACTTA 900
 Db 841 TTGTAAAAAATTGATCAAATCTGCTAAGTGTGAAAGATCAGCGACTTA 900
 Qy 901 GTAGCCTTTAGAAAAATAG 921
 Db 901 GTAGCCTTTAGAAAAATAG 921

Qy 921 ATGAAAGAAGCCCTGCAAAAAGCTTCTGAACTTGGTACTCCAGCCAACTATAAC 480
 Db 921 ATGAAAGAAGCCCTGCAAAAAGCTTCTGAACTTGGTACTCCAGCCAACTATAAC 480
 Qy 481 ACACCTGACAAATCTGCTCTGAGCTTGTGACTCTGAGCTGTTGAACTTT 540
 Db 481 ACACCTGACAAATCTGCTCTGAGCTTGTGACTCTGAGCTGTTGAACTTT 540
 Qy 541 TTGCAAGAGCCTGCAAAACGCTTGTGACTCTGAGCTGTTGAACTTT 600

APPLICANT: Carr, Grant J.
 APPLICANT: Xu, H. Howard
 APPLICANT: Foulkes, J. Gordon
 APPLICANT: Zamudio, Carlos
 APPLICANT: Hasselbeck, Robert
 APPLICANT: Ohisen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Travick, John D.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Roemer, Terry
 APPLICANT: Jiang, Bo
 APPLICANT: Boone, Charles
 APPLICANT: Bussey, Howard
 APPLICANT: Bussey, Howard
 APPLICANT: Methods for Identifying the Target of a Compound which Inhibits
 TITLE OF INVENTION: Proliferation
 FILE REFERENCE: ELITRA.028A
 CURRENT APPLICATION NUMBER: US/10/072,851
 CURRENT FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 1581
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 9482
 LENGTH: 921
 TYPE: DNA
 ORGANISM: *streptococcus pneumoniae*
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(921)
 US-10-072-851-9482

Query Match Score 911.4; DB 39; Length 921;
 Best Local Similarity 99.3%; Pred. No. 2.2e-268;
 Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGACTAAACAGCCTTTTATTGCTGGCCAGTATCTAGGGATGGAA 60
 Db 1 ATGACTAAACAGCCTTTTATTGCTGGCCAGTATCTAGGGATGGAA 60
 Qy 61 GATTCTATGATTGCTCTATCTCATGATCAGAACAGATGATCAGGGCTC 120
 Db 61 GATTCTATGATTGCTCTATCTCATGATCAGAACAGATGATCAGGGCTC 120
 Qy 121 GGTTATGTTACCTTATCTCATGATCAGAACAGATGATCAGGGCTC 180
 Db 121 GGTTATGTTACCTTATCTCATGATCAGAACAGATGATCAGGGCTC 180
 Qy 181 ACGAACACGCCATTCTACGACTCTGGTTGATCAGCTTATTGCAAGAAAGGGC 240
 Db 181 ACGAACACGCCATTCTACGACTCTGGTTGATCAGCTTATTGCAAGAAAGGGC 240
 Qy 241 TATAGCCTGATATGGTCTGGTTGCTGGAAACCTTATGGAA 300
 Db 241 TATAGCCTGATATGGTCTGGTTGCTGGAAACCTTATGGAA 300
 Qy 301 GGCCCTTGATTGATGAGATGGCTTCCCTTGATGGCTTAAGGATACTCTGCTGGTCAAGGTGCCAGTATGGATGGACCG 360
 Db 301 GGCCCTTGATTGATGAGATGGCTTCCCTTGATGGCTTAAGGATACTCTGCTGGTCAAGGTGCCAGTATGGATGGACCG 360
 Qy 361 GAAACGGCTTCCTGTGATCTGCAAGTGGTAACTCCAGTAACTAC 420
 Db 361 GAAACGGCTTCCTGTGATCTGCAAGTGGTAACTCCAGTAACTAC 420
 Qy 421 ATTGAAAGAAAGCCTGTCAAAAGCTTCTGAACTTGGTTTACTCCAGCAACTATAC 480
 Db 421 ATTGAAAGAAAGCCTGTCAAAAGCTTCTGAACTTGGTTTACTCCAGCAACTATAC 480
 Qy 481 ACACCTGACAAATCTGATTGTGGAAAGGGTGAAGTGTATCGCGTTGAACCT 540
 Db 481 ACACCTGACAAATCTGATTGTGGAAAGGGTGAAGTGTATCGCGTTGAACCT 540
 Qy 541 TTGAAGAAGCAGTGCACAACTCCCTTCAACCC 600
 Db 541 TTGAAGAAGCAGTGCACAACTCCCTTCAACCC 600
 Qy 601 GCTCTCCCTGAGCCTGCTAGCCAAAGAAACTAGCTGAAACTCTAGCTGAAAGTTTCA 660
 Db 601 GCTCTCCCTGAGCCTGCTAGCCAAAGAAACTAGCTGAAACTCTAGCTGAAAGTTTCA 660
 Qy 661 GATTTTACCTTGTGCTCTAGTCGCAAAATCAGAAAGCTGTGTGATGAAAGGAGGATT 720
 Db 661 GATTTTACCTTGTGCTCTAGTCGCAAAATCAGAAAGCTGTGTGATGAAAGGAGGATT 720
 Qy 721 GCTCAGCCCTTGAGCCCTGAGCTCAAGGAAACCGCTTCTATGAAAGTATGGCT 780
 Db 721 GCTCAGCCCTTGAGCCCTGAGCTCAAGGAAACCGCTTCTATGAAAGTATGGCT 780
 Qy 781 ATGGAAGAAGCAGCATAGCAACTTATCTGAGATTGACCCGGAAAGTCTTGTCAAGT 840
 Db 781 ATGGAAGAAGCAGCATAGCAACTTATCTGAGATTGACCCGGAAAGTCTTGTCAAGT 840
 Qy 841 TTGTAAAAAATTGATCAAATCTGCTAAGTGTGAAAGATCAGCGACTTA 900
 Db 841 TTGTAAAAAATTGATCAAATCTGCTAAGTGTGAAAGATCAGCGACTTA 900
 Qy 901 GTAGCCTTTAGAAAAATAG 921
 Db 901 GTAGCCTTTAGAAAAATAG 921

APPLICANT: Carr, Grant J.
 APPLICANT: Xu, H. Howard
 APPLICANT: Foulkes, J. Gordon
 APPLICANT: Zamudio, Carlos
 APPLICANT: Hasselbeck, Robert
 APPLICANT: Ohisen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Travick, John D.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Roemer, Terry
 APPLICANT: Jiang, Bo
 APPLICANT: Boone, Charles
 APPLICANT: Bussey, Howard
 APPLICANT: Bussey, Howard
 APPLICANT: Methods for Identifying the Target of a Compound which Inhibits
 TITLE OF INVENTION: Proliferation
 FILE REFERENCE: ELITRA.028A
 CURRENT APPLICATION NUMBER: US/10/072,851
 CURRENT FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 1581
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 9482
 LENGTH: 921
 TYPE: DNA
 ORGANISM: *streptococcus pneumoniae*
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(921)
 US-10-072-851-9482

Query Match Score 911.4; DB 39; Length 921;
 Best Local Similarity 99.3%; Pred. No. 2.2e-268;
 Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGACTAAACAGCCTTTTATTGCTCTCAAGGTGCCAATCTTGGATGGACGG 60
 Db 1 ATGACTAAACAGCCTTTTATTGCTCTCAAGGTGCCAATCTTGGATGGACGG 60
 Qy 61 GATTCTATGATCAGTATTCGATGTCAGGGAGTGGCTAGGTGAACTTT 120
 Db 61 GATTCTATGATCAGTATTCGATGTCAGGGAGTGGCTAGGTGAACTTT 120
 Qy 121 GGTTATGTTACCTTATCTCATGATCAGAACAGATGATCAGGGCTC 180
 Db 121 GGTTATGTTACCTTATCTCATGATCAGAACAGATGATCAGGGCTC 180
 Qy 181 ACGAACACGCCATTCTACGACTCTGGTTGATCAGCTTATTGCAAGAAAGGGC 240
 Db 181 ACGAACACGCCATTCTACGACTCTGGTTGATCAGCTTATTGCAAGAAAGGGC 240
 Qy 241 TATAGCCTGATATGGTCTGGTTGCTGGAAACCTTATGGAA 300
 Db 241 TATAGCCTGATATGGTCTGGTTGCTGGAAACCTTATGGAA 300
 Qy 301 GGCCCTTGATTGATGAGATGGCTTCCCTTGATGGCTTAAGGATACTCTGCTGGTCAAGGTGCCAGTATGGAA 360
 Db 301 GGCCCTTGATTGATGAGATGGCTTCCCTTGATGGCTTAAGGATACTCTGCTGGTCAAGGTGCCAGTATGGAA 360
 Qy 361 ATGAAAGAAGCCTGTCAAAAGCTTCTGAACTTGGTACTCCAGCCAACTATAAC 420
 Db 361 ATGAAAGAAGCCTGTCAAAAGCTTCTGAACTTGGTACTCCAGCCAACTATAAC 420
 Qy 421 ACACCTGACAAATCTGCTAAGTGTGAAAGATCAGCGACTTA 480
 Db 421 ACACCTGACAAATCTGCTAAGTGTGAAAGATCAGCGACTTA 480
 Qy 481 ATGAAAGAAGCCTGTCAAAAGCTTCTGAACTTGGTACTCCAGCCAACTATAAC 540
 Db 481 ATGAAAGAAGCCTGTCAAAAGCTTCTGAACTTGGTACTCCAGCCAACTATAAC 540
 Qy 541 TTGCAAGAGCCTGCAAAACGCTTGTGACTCTGAGCTGTTGAACTTT 600

RESULT 10
 US-10-072-851-9482
 Sequence 9482, Application US/10072851
 GENERAL INFORMATION:

TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 PCT-US97-22578-43

Query Match 99.0%; Score 911.4; DB 1; Length 3580;
 Best Local Similarity 99.3%; Pred. No. 4.1e-268;
 Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGACTAAACAGCCTTTATTTGGTGTAAAGGCCCCAGTATCAGGGATGCGACGG 600
 Db 601 GCTCTCTGAGCTTCTAGCCAAACTAGCTGAAACTTACTGCTTAAAGTCTTCACAC 600
 Qy 601 GCTCTCTGAGCTTCTAGCCAAACTAGCTGAAACTTACTGCTTAAAGTCTTCACAC 600
 Db 601 GATTTTACTCTCCCTATGCGGAAATACAGAAAGTGTGTGATGCAAAGGACAT 720
 Qy 661 GATTTTACTCTCCCTATGCGGAAATACAGAAAGTGTGTGATGCAAAGGACAT 720
 Db 720 GCTAGCTCTGCTGCGTCAAGGAACCCGTCGGTTCTATGAAAGTATGGGCTC 780
 Qy 720 GCTAGCTCTGCTGCGTCAAGGAACCCGTCGGTTCTATGAAAGTATGGGCTC 780
 Db 780 GATGCAAGAGGCAATAGACAGTAACTTACAGATGAAAGTAAAGGACAT 840
 Qy 780 GATGCAAGAGGCAATAGACAGTAACTTACAGATGAAAGTAAAGGACAT 840
 Db 781 ATGCAAGAGGCAATAGACAGTAACTTACAGATGAAAGTAAAGGACAT 840
 Qy 781 ATGCAAGAGGCAATAGACAGTAACTTACAGATGAAAGTAAAGGACAT 840
 Db 840 GCTAGCTCTGCTGCGTCAAGGAACCCGTCGGTTCTATGAAAGTATGGGCTC 897
 Qy 840 GCTAGCTCTGCTGCGTCAAGGAACCCGTCGGTTCTATGAAAGTATGGGCTC 897
 Db 841 ATGCAAGAGGCAATAGACAGTAACTTACAGATGAAAGTAAAGGACAT 900
 Qy 841 ATGCAAGAGGCAATAGACAGTAACTTACAGATGAAAGTAAAGGACAT 900
 Db 900 GATGCAAGAGGCAATAGACAGTAACTTACAGATGAAAGTAAAGGACAT 900
 Qy 900 GATGCAAGAGGCAATAGACAGTAACTTACAGATGAAAGTAAAGGACAT 921
 Db 921 GATGCAAGAGGCAATAGACAGTAACTTACAGATGAAAGTAAAGGACAT 921

RESULT 11
 PCT-US97-22578-43
 / Sequence 4.3, Application PC/TUS9722578

/ GENERAL INFORMATION:
 / APPLICANT: Balt, Richard H.
 / APPLICANT: Burgett, Stanley G.
 / APPLICANT: Dehoff, Bradley S.
 / APPLICANT: Jeskunas Jr., Stanley R.
 / APPLICANT: Mills, Bradley J.
 / APPLICANT: Peery, Robert B.
 / APPLICANT: Rosteck Jr., Paul R.
 / APPLICANT: Shatrid, Paul L.
 / APPLICANT: Smith, Michele C.
 / APPLICANT: Rockey, Pamela K.
 / APPLICANT: Young-Bellido, Michele

/ TITLE OF INVENTION: Streptococcus Pneumoniae DNA Sequences
 / NUMBER OF SEQUENCES: 228
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Eli Lilly and Company
 / STREET: Lilly Corporate Center
 / CITY: Indianapolis
 / STATE: Indiana
 / COUNTRY: U.S.
 / ZIP: 46285
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: FLOPPY DISK
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: PCT/US97/22578
 / FILING DATE:
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Webster, Thomas D.
 / REGISTRATION NUMBER: X-11162
 / REFERENCE/DOCKET NUMBER: 39-A72
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 317-276-3334
 / INFORMATION FOR SEQ ID NO: 43:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 3580 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / 901 GTAGCACTTTAGAAATAAG 921
 / 1618 GTAGCACTTTAGAAATAAG 1618

RESULT 12
 S-60-068-175-555
 Sequence 555, Application US/60068175
 GENERAL INFORMATION:
 APPLICANT: Lagace, Robert E.
 APPLICANT: Corley, Neil C.
 APPLICANT: Russo, Frank D.
 APPLICANT: Hann, Amy L.
 APPLICANT: Heath, Joe D.
 APPLICANT: Finney, Gregory L.
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
 TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
 NUMBER OF SEQUENCES: 1175
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/60/066,175
 FILING DATE: HEREWITH
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: CERRONE, MICHAEL C.
 REGISTRATION NUMBER: 39 132
 REFERENCE/DOCKET NUMBER: PM-0009-2 P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 INFORMATION FOR SEQ ID NO: 555:
 LENGTH: 9753 base pairs
 STRANDDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: Genomic DNA
 IMMEDIATE SOURCE:
 CLONE: SPN2C557
 S-60-068-175-555
 Query Match 99.0%; Score 911.4; DB 50; Length 9753;
 Best Local Similarity 99.3%; Pred. No. 6.5e-268;
 Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Y 1 ATGACTAAACAGCCTTATTGCTGTTCAAGGTGCCAATCTGAGGATGGACGG 60
 o 1234 ATGACTAAACAGCCTTATTGCTGTTCAAGGTGCCAATCTGAGGATGGACGG 1293
 Y 61 GATTCTCATGATGATTCGATTGTCAAAGAACGATGATGAGCAGTGGCTC 120
 o 1294 GATTCTCATGATGATTCGATTGTCAAAGAACGATGATGAGCAGTGGCTA 1353
 Y 121 GGTTATGATTACGTTACCTATCATGATGAGAACGAAACTCATGAGCAGTGGCT 180
 o 1354 GGTTATGATTGCTTACATGATGAGAACGAAACTCATGAGCAGTGGCTA 1413
 Y 181 ACGCAACAGCCATTCTGAGCTTCTGGAGATACTCTGGAGATACTCTGGCTTGGCT 300
 o 1414 ACGCAACAGCCATTCTGAGCTTCTGGAGATACTCTGGCTTGGCT 1473
 Y 241 TATGAGCTGATAGTTCTGGACTCTGGAGATACTCTGGCTTGGCT 300
 o 1474 TATGAGCTGATAGTTCTGGACTCTGGCTTGGCT 1533

RESULT 13
 US-09-752-069A-256
 ; Sequence 256, Application US/09752069A
 ; GENERAL INFORMATION:
 ; APPLICANT: Dougherty, Thomas J.
 ; APPLICANT: Pucci, Michael J.
 ; APPLICANT: Dougherty, Brian A.
 ; APPLICANT: Davison, Daniel B.
 ; APPLICANT: Bruccoleri, Robert E.
 ; APPLICANT: Thanassi, Jane A.
 ; APPLICANT: Farmer II, Bennett T.
 ; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
 ; APPLICANT: Dougherty, Thomas J.
 ; APPLICANT: Pucci, Michael J.
 ; APPLICANT: Dougherty, Brian A.
 ; APPLICANT: Davison, Daniel B.
 ; APPLICANT: Bruccoleri, Robert E.
 ; APPLICANT: Thanassi, Jane A.
 ; APPLICANT: Farmer II, Bennett T.
 ; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
 ; APPLICANT: Dougherty, Thomas J.
 ; APPLICANT: Pucci, Michael J.
 ; APPLICANT: Dougherty, Brian A.
 ; APPLICANT: Davison, Daniel B.
 ; APPLICANT: Bruccoleri, Robert E.
 ; CURRENT FILING DATE: 2000-12-29
 ; PRIORITY APPLICATION NUMBER: 60/174,089
 ; PRIORITY FILING DATE: 1999-12-30
 ; NUMBER OF SEQ ID NOS: 338
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 256
 ; LENGTH: 945
 ; TYPE: DNA
 ; ORGANISM: Streptococcus pneumoniae
 ; US-09-752-069A-256
 ; Query Match 98.6%; Score 908.4; DB 29; Length 945;
 ; PCT LOCAL SIMILARITY 99.2%; PRED NO. 1.9e267;

Matches 912; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGACTAACGCCCTTTTATTGCGTCAGGCCAGTATAGGGATGGACGG 60
 Db 1 ATGACTAACGCCCTTTTATTGCGTCAGGCCAGTATAGGGATGGACGG 60
 Qy 61 GATTCTATGATCACTATCGATTGTCAAGAACGATGATCGACCGAGTCAGGTGCTC 120
 Db 61 GATTCTATGATCACTATCGATTGTCAAGAACGATGATCGACCGAGTCAGGTGCTC 120
 Qy 121 CGITTAATTAGTTATCTCATGATAAGAGAACAAACTCAATCGACCGCTAT 180
 Db 121 CGITTAATTAGTTATCTCATGATAAGAGAACAAACTCAATCGACCGCTAT 180
 Qy 181 AGGCAACAGCCATTAGCAGCTTCTAGCAGCTCGTGTCTATACCGTTATTGAGAAGGGC 240
 Db 181 AGGCAACAGCCATTAGCAGCTTCTAGCAGCTCGTGTCTATACCGTTATTGAGAAGGGC 240
 Qy 241 TATCGCCTGATATGGTGTGGTTGTCTTGGAGATACTCGCTTGGCAGC 300
 Db 241 TATCGCCTGATATGGTGTGGTTGTCTTGGAGATACTCGCTTGGCAGC 300
 Qy 301 GGCGCCTGGATTGAGATCGGGTCCGTGAGCTTACGGTAACTATGGAA 360
 Db 301 GGCGCCTGGATTGAGATCGGGTCCGTGAGCTTACGGTAACTATGGAA 360
 Qy 361 GAAGGGCTCCCTGACTCTGGCAGATGCTAGGTTCTCAATACGCCAGTGGCTC 420
 Db 361 GAAGGGCTCCCTGACTCTGGCAGATGCTAGGTTCTCAATACGCCAGTGGCTC 420
 Qy 421 ATTGAGAGAACGCTGTCAAAGCTCTGAACTTGGTGTCTCCAGCAACTATAAC 480
 Db 421 ATTGAGAGAACGCTGTCAAAGCTCTGAACTTGGTGTCTCCAGCAACTATAAC 480
 Qy 481 ACACCTGCAACATCGTAACTGAGAAGCTGGAGTGTGAGTGTGAGCT 540
 Db 481 ACACCTGCAACATCGTAACTGAGAAGCTGGAGTGTGAGTGTGAGCT 540
 Qy 541 TTGCAAGAGACGGTGCAGAACGGTGTAACTCTCTGAAGGTGCTGAGTGTGAGCT 600
 Db 541 TTGCAAGAGACGGTGCAGAACGGTGTAACTCTCTGAAGGTGCTGAGTGTGAGCT 600
 Qy 601 GCTCTCCCTGAGCTCTGAGCTTCAAGCTTCTAGCTCAAGTAAAGTCTCA 660
 Db 601 TCTCTCCCTGAACTCTGAGCTTCAAGCTTCTAGCTCAAGTAAAGTCTCA 660
 Qy 661 GATTTTACTTGCCTAGTGGCATACTAGAAGTGTCTGATGCAAAAGAGACATT 720
 Db 661 GATTTTACTTGCCTAGTGGCATACTAGAAGTGTCTGATGCAAAAGAGACATT 720
 Qy 721 GCTCAGCTCTGAGCCGCTAGTCAAGAACCGTCTGTTCTAGAAACTATGGGTG 780
 Db 721 GCTCAGCTCTGAGCCGCTAGTCAAGAACCGTCTGTTCTAGAAACTATGGGTG 780
 Qy 781 ATGCAAGAGCGGCTAGGACTTTATCGAGATGGACGGAAAGCTTGTGAGT 840
 Db 781 ATGCAAGAGCGGCTAGGACTTTATCGAGATGGACGGAAAGCTTGTGAGT 840
 Qy 841 TTGTTAAAAAATTGATCAAATCTGCTCAACTAGCTCATGTTGAAGATCAAGCAGTTA 900
 Db 841 TTGTTAAAAAATTGATCAAATCTGCTCAACTAGCTCATGTTGAAGATCAAGCAGTTA 900
 Qy 901 GTAGCACTTTAGAAAA 916
 Db 901 GTAGCACTTTAGAAAA 916
 Qy 301 GGCCCTTGGATTGAGATGGTGGCTTACGGTAACTGTTGCTTATGGAA 360
 Db 3219 GGCGCTGGATTGAGATGGTGGCTTACGGTAACTGTTGCTTATGGAA 3278
 Qy 361 GAGGGGTCCTGCTGACTCTGCAAGATGGTAGCTGCTGAGCTATAGGGTC 420
 Db 3279 GAGGGGTCCTGCTGACTCTGCAAGATGGTAGCTGCTGAGCTATAGGGTC 3388

APPLICANT: RUSSO, FRANK D.
 APPLICANT: HANN, AMY L.
 APPLICANT: HEATH, JOE D.
 APPLICANT: FINNENY, GREGORY L.
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
 NUMBER OF SEQUENCES: 797
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/60/061,998
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: CERONE, MICHAEL C.
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PM-0006-2P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 494:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5963 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: SPN1C499
 US-60-061-998-494

Query Match 96.8%; Score 891.6; DB 50; Length 5963;
 Best Local Similarity 98.9%; Pred. No. 6.2e-22;
 Matches 908; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 1 ATGACTAACAGCTTTTATTGCGTCAGGTGCCAGTATCTGGATGGACGG 60
 Db 2919 ATGACTAACAGCTTTTATTGCGTCAGGTGCCAGTATCTGGATGGACGG 2978
 Qy 61 GATTTCTATGATCACTGCTGAGTATCCGATTGTCAGGTGCCAGTATCTGGATGGACGG 120
 Db 2979 GATTTCTATGATCACTGCTGAGTATCCGATTGTCAGGTGCCAGTATCTGGATGGACGG 3098
 Qy 121 GGTTATGATTTAGTTTCTGATGAACTCAATCAGGCCGCTAT 180
 Db 3039 GGTTATGATTTGGTTATCTCATGATACGGAAAGAAACTCTGATGAACTCAATCAGGCCGCTAT 3098
 Qy 181 ACGCAACAGCCATTAGGACTTCTAGGACTTCTGGTATCTACCGTTATGGCAAAAGGGC 240
 Db 3099 ACGCAACAGCCATTAGGACTTCTAGGACTTCTGGTATCTACCGTTATGGCAAAAGGGC 3158
 Qy 241 TATGAGCTGATATGGTGTGGTTCTCTGGAGAATACTGCTCTGGTGGAACT 300
 Db 3159 TATGAGCTGATATGGTGTGGTTCTCTGGAGAATACTGCTCTGGTGGAACT 3218

RESULT 14
 US-60-061-998-494
 Sequence 94, Application US/60061998
 GENERAL INFORMATION:
 APPLICANT: LAGAE, ROBERT E.
 APPLICANT: CORLEY, NEIL C.

Qy 421 ATTGAGAACGCTGTCAAAAGCTCTGAACTGGAGGTTACTCCAGCCAACTATAAC 480
 Db 3339 ATTGAGAACGCTGTCAAAAGCTCTGAACTGGAGGTTACTCCAGCCAACTATAAC 3398
 Qy 481 ACACCT-GCAAAATGCTCATTCGAGAGTGGAGTTGAGTTGAACTTGGAGTAAAC 539
 Db 3399 ACACCTGGCAAAATGCTCATTCGAGAGTGGAGTTGAACTTGGAGTAAAC 3458
 Qy 540 TTGCAAGAACGAGCTGCAAAACGGTGAAGGTGCAAGTCCTTAACTGCAAC 599
 Db 3459 TTGCAAGAACGAGCTGCAAAACGGTGAAGGTGCAAGTCCTTAACTGCAAC 3518
 Qy 600 CGCTCTCTGTAGCCAGAAACTAGCTGAAACTAGCTAGCTAGGTAAAGTTTC 659
 Db 3519 CTCTCTGTAGCCAGAAACTAGCTGAAACTAGCTAGGTAAAGTTTC 3578
 Qy 660 AGATTTACTGTCCCTAGTCGGAAAGAGGAAAT 719
 Db 3579 AGATTTACTGTCCCTAGTCGGAAAGAGGAAAT 3638
 Qy 720 TGCTCAGCTCTGAGGGTAGGTCAGGTCAGGAAACCGTTCTTTCTGAAAGTATTGGGT 779
 Db 3639 TGCTCAGCTCTGAGGGTAGGTCAGGAAACCGTTCTTTCTGAAAGTATTGGGT 3698
 Qy 780 CATGAAAGAGCAGGCAATGAAACTTTATGAGATGACCGGGAAAGTCTGTGAGG 839
 Db 3699 CATGAAAGAGCAGGCAATGAACTTTATGAGATGACCGGGAAAGTCTGTGAGG 3758
 Qy 840 TTGGTTAAAAAATTGATAAACTGCTCATGGAAAGGT 899
 Db 3759 TTGGTTAAAAAATTGATAAACTGCTCATGGAAAGGT 3818
 Qy 900 AGTAGGCACTTTAGAAAA 917
 Db 3819 AGTAGGCACTTTAGAAAA 3836

Search completed: June 11, 2003, 19:45:30
 Job time : 2192 secs

RESULT 15
 US-09-308-397-5
 Sequence 5, Application US/09308397
 GENERAL INFORMATION:
 APPLICANT: Gentry, Daniel R.
 APPLICANT: Lonsdale, John T.
 APPLICANT: Payne, David J.
 APPLICANT: Pearson, Stewart C.
 APPLICANT: Van Aller, Glenn C.
 TITLE OF INVENTION: Novel FabD
 FILE REFERENCE: P50593
 CURRENT APPLICATION NUMBER: US/09/308,397
 EARLIER FILING DATE: 1999-05-18
 EARLIER APPLICATION NUMBER: US 60/031,160
 EARLIER FILING DATE: 1996-11-18
 EARLIER APPLICATION NUMBER: PCT/US97/20992
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5
 LENGTH: 547
 TYPE: DNA
 ORGANISM: Streptococcus pneumoniae
 US-09-308-397-5

Query Match 57.5%; Score 529.4; DB 17; Length 547;
 Best Local Similarity 98.0%; Pred. No. 3.8e-151; Mismatches 11; Indels 0; Gaps 0;
 Matches 536; Conservative 0;

Qy 372 TGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGGCAAGTAGGGCATGGAGAGC 431
 Db 1 TGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGGCAAGTAGGGCATGGAGAGC 60
 Qy 432 CTGTCAAAAGCTCTGAACTTGGAGGTTACTCCAGCAACTATAACACTGCPCA 491
 Db 61 CTGTCAAAAGCTCTGAACTTGGAGGTTACTCCAGCAACTATAACACCTGCPCA 120

23	168	18.2	930	9	US-10-282-122A-38967	Sequence 38967, A	
	166	18.1	942	8	US-10-369-493-41012	Sequence 41012, A	
	225	18.0	2301	9	US-10-398-121-3159	Sequence 3519, AP	
	165	17.9	930	9	US-10-282-122A-12230	Sequence 42230, A	
	226	17.8	227	9	US-10-282-122A-19704	Sequence 39704, A	
	164	17.8	930	9	US-10-194-163A-003	Sequence 1003, AP	
	228	17.9	9686	8	US-10-194-163-1003	Sequence 1003, AP	
	164	17.9	9686	9	US-10-194-163-1003	Sequence 1003, AP	
	229	17.9	9686	9	US-10-398-221-7	Sequence 7, Appl. 11	
	162	17.6	319630	8	US-10-398-221-2058	Sequence 2058, AP	
	30	162.4	17.6	3011208	8	US-10-282-122A-4478	Sequence 24478, A
	331	162.4	17.6	942	9	US-10-282-122A-23167	Sequence 23167, A
	332	160.4	17.4	926	9	US-10-282-122A-1669	Sequence 31669, A
	165	17.2	1092	9	US-10-282-122A-1669	Sequence 31669, A	
	334	15.7	10.0	918	8	US-10-369-493-4861	Sequence 42861, A
	335	15.6	16.5	918	8	US-10-369-493-4861	Sequence 42861, A
	336	14.9	16.5	9	US-10-282-122A-16638	Sequence 36638, A	
	337	14.2	14.5	948	9	US-10-282-122A-17057	Sequence 17057, A
	338	14.0	15.2	945	9	US-10-282-122A-5339	Sequence 25339, A
	339	13.9	15.1	843	8	US-10-369-493-3918	Sequence 33918, A
	40	13.7	14.9	771	8	US-10-446-203-272	Sequence 272, AP
	41	13.6	14.8	2272325	9	US-10-018-470A-1	Sequence 1, Appl. 1
	42	13.6	14.8	2272325	9	US-10-018-470A-1	Sequence 1, Appl. 1
	43	13.4	14.6	885	9	US-10-282-122A-2672	Sequence 12672, A
	44	13.3	14.6	942	9	US-10-282-122A-0998	Sequence 9998, AP
	45	13.3	14.5	927	9	US-10-282-122A-59553	Sequence 29553, A

ALIGNMENTS

Pending Patents NA New: *

1: /cgm1_6/podata/1/pna/US07_NW_COMB.seq: *

2: /cgm1_6/podata/1/pna/US06_NW_COMB.seq: *

3: /cgm2_6/podata/1/pna/US07_NW_COMB.seq: *

4: /cgm2_6/podata/1/pna/US08_NW_COMB.seq: *

5: /cgm2_6/podata/1/pna/US09_NW_COMB.seq: *

6: /cgm2_6/podata/1/pna/US10_NW_COMB.seq: *

7: /cgm2_6/podata/1/pna/US11_NW_COMB.seq: *

8: /cgm2_6/podata/1/pna/US12_NW_COMB.seq: *

9: /cgm2_6/podata/1/pna/US05_NW_COMB.seq: *

10: /cgm2_6/podata/1/pna/US60_NW_COMB.seq: *

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

SUMMARIES

Score	No.
911.4	1
459.4	2
439.3	3
388.8	4
350.8	5
350.8	6
350.8	7
316.8	8
316.8	9
315.2	10
217.6	11
196.4	12
196.4	13
196.4	14
196.4	15
c	16
c	17
c	18
c	19
c	20
c	21
c	22

Description	
Sequence 37621, A	
Sequence 36004, A	
Sequence 38525, A	
Sequence 42057, A	
Sequence 20712, A	
Sequence 1582, AP	
Sequence 1582, AP	
Sequence 1582, AP	
Sequence 21491, A	
Sequence 41191, A	
Sequence 32186, A	
Sequence 21907, A	
Sequence 1, APP11	
Sequence 1, APP11	
Sequence 364, APP11	
Sequence 24480, A	
Sequence 20335, A	
Sequence 46809, A	
Sequence 31257, A	
Sequence 15949, A	
Sequence 16221, A	

Qy 721 GCTCAGCTCTGACGGCTCAGGAAACCGTTCTATGAAGTATTGGGTC 780
 Db 721 CCAGAACTTATAGCCCGTCAGTCAGTCAGGAACTGGCTTTATGACAGTGTGGCACT 780
 Qy 781 ATGCAAGAAGCAGGATTAAGCAACCTTATGAGATTGGACGGAAAGTCAGTGTGGAGT 840
 Db 781 TTAGPAGAATGTCATACAAATCAATGAGTAAAGCCAGTAAAGTTGACAGT 840
 Qy 841 TTGGTTAAAAAATTGATCAAAACTGCTCACTTAGGTCTATGTTGAAAGTCAAGGGATTA 900
 Db 841 TTGGAGAGAAATGATTAATTAATGACTATGACTATGTTGAAACATGTAAGCTTA 900
 Qy 901 GTAGCACTTTAGAAAAATAG 921
 Db 901 CGTTTATTTAGATAGAGAG 921

RESULT 4
 US-10-369-4-93-42057
 Sequence 20712, Application US/10369493
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-10152052 B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO: 42257
 LENGTH: 927
 TYPE: DNA
 ORGANISM: Lactococcus lactis

US-10-369-4-93-42057

Query Match 42.2%; Score 388.8; DB 8; Length 927;
 Best Local Similarity 64.6%; Pred. No. 7.3e-109; Mismatches 322; Indels 6; Gaps 1;
 Matches 598; Conservative 0;

Qy 1 ATGACTAAACAGCCTTATTGCTGTCAGGTCAGTATCTGGATGGACCG 60
 Db 1 ATGACTAAACAGCATTATCTCAGCTCAAGGGCAAAAGCTGGAAATGGACGT 60
 Qy 61 GATTCTATGATCAGTATCGATGTCAGAACGATGTGATCGAGTCGGTC 120
 Db 61 GACTATATGHCACCATATGAAACAGTAAAGCAACTTGTGAAAGCAGCTTA 120
 Qy 121 GGTTATGATTACGTTCTCATGATACGGAAACCTCATAGACCCGAT 180
 Db 121 GGATATGATTGGAGCTTGTGATGATAATGATAGAAACAAAGTAC 180
 Qy 181 ACGCCAACAGCCTTCAGGACATTCAGGTCAGTCTACCGTTATGGCAAGGC 240
 Db 181 ACTCAACTGCAATTTAACACCTCTGTCATTTAGTGTGTTAGTGAATGG 240
 Qy 241 TATCAGCCTGATATGGTTGCTGTTGAGATAACTCTGGAGCTTATGGCAAGGC 300
 Db 241 ATTAACCTGACCTTGTGTTAGTGTGTTAGTGTGTTAGTGTGTTAGCATCA 300
 Qy 301 GGGCCTGGAATTTCAGAGATGGCTTGGCTCTGGAGATAACTCTGGAGCTTATGGCAAGGC 360
 Db 301 GGAATATGATTTCAGAGACCTTAACCTGTCATATGGCAATATGGCA 360
 Qy 361 GAAAGCCTCTGCTGACTCTGGCAAGATGGTAGGAGTCATACGCCAGTAGGGTC 420
 Db 361 GAAAGCCTGACCGACTGGTCGGTAAATGGACACAGACCCAGCCTG 420
 Qy 421 ATGGAGAAGCCTGTCAAAAGCTCTGAACCTTGTGTTACTCCAGCAAC 474

Db 421 ATTGAGAAATTGGCAAGGCCGATTAAGGGGTATTGTTAGTCCAGCAAAAT 480
 Qy 475 TATAGACNCACCTGCCAAATCCTGCTTGGAGAGGGTTGAGTTGATCGAGCGGT 534
 Db 481 TATAAGCAGCCGCAAAATGTTGTTGTTGAGGGTTGTTATTGCTGTT 540
 Qy 535 GAACTTTGCAAGAGCAGGTCAGGTCACCTGTTCTTAAGGTGTCAGGTCCTT 594
 Db 541 GAGTGTCTAAAGAGCCGGAGTTGTAACCTPATGAAATTAAAGTTTCAGGACCTTC 600
 Qy 595 CACACGGCTTCCTGAGCTGAGCCGAAACTAGCTGAAACTCTAAGTCAAGTAAAG 654
 Db 601 CATAZGCAATTTTAAACCAAGCATCTGAAATTGGGTTGGAGCTTATGAAATTGAT 660
 Qy 655 TTTTCAGATTTCATTGTCCTTGTGAAATTCAATGAGTGTGCTAAAGTCAAGTAAAG 714
 Db 661 TTAGACCTTTGAAATTACATTAACTCTCAATGAGTGTGCTAAAGTAAATGAT 720
 Qy 715 GACATTCGTCAGCTCTGAGCGCTTGAAGGAAACCGGTCGTTCTATGAAAGTATT 774
 Db 721 GAAGTAAAGGACTTTGAGCGTAAAGTATGGACCTGTTTGTGAACTGGT 780
 Qy 775 GGGGTCATGCAAGAAGCAGGGCATTAAGCAACTTATGAGATTGGACGGAAAGTCCTG 834
 Db 781 GAAACATGCAAAACTAGGGCGACTGCTGTTTATGAACTGGAGTACT 840
 Qy 835 TCAAGTTTGTGTAAGGAAATGATCAACTGCTCATGTTGAAAGAGTCAGGTCAGT 894
 Db 841 TCAGGTTTCATTAAGGAAATGATGAAATGCAAGAAATTGCTAAATGTTGAAATTGATC 900
 Qy 895 AGTTAGTAGACTTTAGAAATA 920
 Db 901 TCATTTGAAAGTTTGATTAAATCAGTA 926

RESULT 5
 US-10-28-122A-20712
 Sequence 20712, Application US/10282122A
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cherry
 APPLICANT: Baselbeck, Robert
 APPLICANT: Ohissen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITPA_031A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 7814
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 20712
 LENGTH: 927
 TYPE: DNA
 ORGANISM: Enterococcus faecalis
 US-10-282-122A-20712

RESULT 6
 US-09-1134-000C-1582
 ; Sequence 1582, Application US/0913400C
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/1134,000C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIORITY APPLICATION NUMBER: US 60/055,778
 ; PRIORITY FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 1582
 ; LENGTH: 948
 ; TYPE: DNA
 ; ORGANISM: Enterococcus faecalis
 US-09-1134-000C-1582

Query Match 38.1%; Score 350.8; DB 9; Length 927;
 Best Local Similarity 61.7%; Pred. No. 3..8e-97; Mismatches 347; Indels 0; Gaps 0;
 Matches 559; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

7 AAACAGCTTTTATTGCTGGTCAAAGTGGATCTAGGGATGGACGGATTTC 66
 4 AAACAGCTTTATTAGTGGACAAGGAGCCAGATCAGGGATGGAAAGATA 63
 67 TATGATCAGTATCGGATTTCAAGAAACGATGATCCAGGAGTCGGTTAT 126
 64 TATCACCAGAAAGGATGTTCGGGAAACTTCGATGAAGCAAGTATCTTAGTTAT 123
 QY 127 GATTACGGTATCTCATCATACTGAAAGAACATCAATAGACCCGTTATGCCAA 186
 DB 124 GAGTGGAGAACCTTGTGTTATGAAATGAGCTTAAAGAAAGAATAGCAA 183

QY 187 CCAGCCATTCTAGGACTTCGGCTTGTGCTTACCGTTATTGCAAGAAAGGGCTATCAG 246
 DB 184 CCTGTTATTAAAGTCTAGTGTGCAATTACCGTTTGTGAAACAAAGGACTAACG 243
 QY 247 CCTGATATGGTGTGGTTGTCTCTGGAGATACTCTGCCCTGGTCAAAGCGGCC 306
 DB 244 CCTGATGTCAGGGTTAAAGTTAGGGATAACGTGCTTGGTGCCTGGCGGGCT 303

QY 307 TTGGATTGAAAGTGGCTTGGTGGCTAAGCTGGACCCCTATGGAAAGAGCG 366
 DB 304 TTGGCTTTTCAGAGCAGTCAGGCTGGCTTGGTCCAAAGCCGGTCAAGTACAGAGCA 363

QY 367 GCTCCTGCTGACTCTGGAAAGATGGTAGCAGTCTCATACGCCAGTGAAGGTCTATGAA 426
 DB 364 GCACCAACAGGAACTGGTAACTGGCTTCTGAACTTACACACT 423

QY 427 GAAGCTGTCAAAAGCTCTGAAACTTGGTACTCCAGGCCAATCTACACACT 486
 DB 424 AAAGCCTGCAAGAAGCAGTCAGTCTTCCGAAATTGGCCAAATTATAACCA 483

QY 487 GCACAAATGGTCACTGGTGGAGAAGTGGTGTGAACTTTGCAA 546
 DB 484 CARAAATGGTCACTGGTGGGGTGGGTGCTGTGTTCAAGGATGACCTTCACAA 543

QY 547 GAAGCAGGTGCCCCAACGGCTTGTGAACTCTGGTCAAGGTGCTTCACCCGCTCTC 606
 DB 544 GAAGCTGGTGTGAAAGGATGATTCGGTAAATGTGACTGGGGCT 603

QY 607 CTTGAGCCGCTGCTGGAAACTTGGTCAAGTGGTCACTGGTCAAGTTTCAGATT 666
 DB 604 TTAGAACAGCATTCAAAAATGGCTAGGATTAGAAAATGACCTTAAACCTG 663

QY 667 ACTGGTCCCTAGTGGTAAAGGATGCTGTTGAAAGGAGATGGTCAAG 726
 DB 664 CAAATTCTGTCATTAGTAACTGCACTGGCAAAATTAGGCCCAAGGGCAATTCAAGCG 723

QY 727 CTCTGTGCACTGGTCAAGTGGACCCGGTCTGTTGCAAGTGGTCACTGGTCAAG 786
 DB 724 TTATGGAAAGGACTATGGTCAAGTGGTCACTGGTCACTGGTCAAG 783

QY 787 GAAGCAGGCTAAAGCAACTTATGGATGAGTGGACCCGGAAACTCTTCAGTT 846
 DB 784 GCTATGAAGCTGAAAGGATGATGAAAGTGGTCAAGGAAACATTAACCTGGTT 843

QY 847 AAAAATTCATCAAACTCTGAACTTGGCAAACTTGGCAACTTGGCAACTTGGCA 906
 DB 844 AAAAATTAATTGACAAATGAAATGACCCGTGTTGGAGATGTTGCACATTAAAGAGA 903

QY 907 CTTITA 912
 DB 904 ACGTTA 909

QY 913 CTTITA 912
 DB 914 ACGTTA 909

QY 915 CTTITA 912
 DB 916 ACGTTA 909

QY 917 CTTITA 912
 DB 918 ACGTTA 909

QY 919 CTTITA 912
 DB 920 ACGTTA 909

QY 921 CTTITA 912
 DB 922 ACGTTA 909

QY 923 CTTITA 912
 DB 924 ACGTTA 909

QY 925 CTTITA 912
 DB 926 ACGTTA 909

QY 927 CTTITA 912
 DB 928 ACGTTA 909

QY 929 CTTITA 912
 DB 930 ACGTTA 909

QY 931 CTTITA 912
 DB 932 ACGTTA 909

QY 933 CTTITA 912
 DB 934 ACGTTA 909

QY 935 CTTITA 912
 DB 936 ACGTTA 909

QY 937 CTTITA 912
 DB 938 ACGTTA 909

QY 939 CTTITA 912
 DB 940 ACGTTA 909

QY 941 CTTITA 912
 DB 942 ACGTTA 909

QY 943 CTTITA 912
 DB 944 ACGTTA 909

QY 945 CTTITA 912
 DB 946 ACGTTA 909

QY 947 CTTITA 912
 DB 948 ACGTTA 909

QY 949 CTTITA 912
 DB 950 ACGTTA 909

QY 951 CTTITA 912
 DB 952 ACGTTA 909

QY 953 CTTITA 912
 DB 954 ACGTTA 909

QY 955 CTTITA 912
 DB 956 ACGTTA 909

QY 957 CTTITA 912
 DB 958 ACGTTA 909

QY 959 CTTITA 912
 DB 960 ACGTTA 909

QY 961 CTTITA 912
 DB 962 ACGTTA 909

QY 963 CTTITA 912
 DB 964 ACGTTA 909

QY 965 CTTITA 912
 DB 966 ACGTTA 909

QY 967 CTTITA 912
 DB 968 ACGTTA 909

QY 969 CTTITA 912
 DB 970 ACGTTA 909

QY 971 CTTITA 912
 DB 972 ACGTTA 909

QY 973 CTTITA 912
 DB 974 ACGTTA 909

QY 975 CTTITA 912
 DB 976 ACGTTA 909

QY 977 CTTITA 912
 DB 978 ACGTTA 909

QY 979 CTTITA 912
 DB 980 ACGTTA 909

QY 981 CTTITA 912
 DB 982 ACGTTA 909

QY 983 CTTITA 912
 DB 984 ACGTTA 909

QY 985 CTTITA 912
 DB 986 ACGTTA 909

QY 987 CTTITA 912
 DB 988 ACGTTA 909

QY 989 CTTITA 912
 DB 990 ACGTTA 909

QY 991 CTTITA 912
 DB 992 ACGTTA 909

QY 993 CTTITA 912
 DB 994 ACGTTA 909

QY 995 CTTITA 912
 DB 996 ACGTTA 909

QY 997 CTTITA 912
 DB 998 ACGTTA 909

QY 999 CTTITA 912
 DB 1000 ACGTTA 909

622 TTAAACCCAGCATCAAAAATGGCTCAGGATTAGAAATTGAAACTTCAACGATG 681
 667 ACITGTCCCCTAGTGGCATACAGAAGTGGCTGTGATCAAAGGACATTGCTAG 726
 682 CAAATTCCCTCATAGTAACTGGCATGCGAAATTGGCCCAAGGCAATTCAACCC 741
 727 CTCTTGAACTGGTAGGCAAGAACCCGTTCTATGAAAGTATTGGCTCATCGAA 786
 742 TTATTGAAAGGAAAGCTGATGTTGAGACGATGTTGAAAGATGAG 801
 787 GAAAGCCGGATTAAGCAACTTATGAGATTGGACGGGCAAACTCTGTCAAGGTT 846
 802 GCPATGAACTGGTAGAACGATGATTGAAAGTTCAGGAAACATTAACCTGTTCTT 861
 847 AAAAAAATGATCAAACCTGTCACCTAGCTCATGTTGAAAGATAAGCCGACTT 906
 862 AAAAAAATGACAAACATGAAATGCAAACTGACCGTGTGGAGATGTGGACATTAACGAA 921
 907 CTTTTA 912
 922 ACGGTTA 927

RESULT 7
 Sequence 1582, Application US/09134000C
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1582
 LENGTH: 948

TYPE: DNA
 ORGANISM: Enterococcus faecalis
 3-09-134-000C-1582

Query Match 38.1%; Score 350.8; DB 6; Length 948;
 Best Local Similarity 61.7%; Pred. No. 3.8e-97;
 Matches 559; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

7 AAAACAGCCTTTTATTGCTGGCTCAAGCTGCCAGPATCTAGGGATGGGACTGGGATTTC 66
 22 AAACAGCCTTTTATTGCTGGCTCAAGCTGCCAGPATCTAGGGATGGGACTGGGATTTC 81
 67 TAATGATCAGTATCCGATGTCAGAACAGATGATCGAGCGTCAAGCTGGCTGGGTAT 126
 82 TATACCCAGAAGGGATGTCGGAAACTTGTGGAGATCTAGATCATTTAGGTAT 141
 127 GATTAGCTTATCTCATACCGAAACTCAATGACCCGTATACGCA 186
 142 GAGATGGAGAACATTGTTTACTGAAATGAGCTTAAATGAAACATACGCAA 201
 187 CCAGCCATTTCTAGGACATCTGGCTGGTGTCTACCGTTATGCAAGAAAGGGCTATAG 246
 202 CCTGCTCATTTAACGTCAGTGTGCAATTACGCTTGTGGCTATACGTTTACGCA 261
 247 CCTGATGTCAGTGTGGCTGGTGTCTACGCTTGTGGCTATACGCTTGTGGCTATACG 306
 262 CCTGATGTCAGTGTGGCTGGTGTCTACGCTTGTGGCTATACGCTTGTGGCTATACG 321
 307 TTGGATTGAGATGGCTGGTGTGGCTGGTGTGGCTGGCTATACGCTTGTGGCTATACG 366
 322 TTGGCTTTCAGAGCAGCTGGCTTGTGGCTCAAGGCGTCAAGGAGGAGGCA 381
 367 GCTCTCTGTCAGTGTGGACTCTGGCAAGATGGTAGCACTGCTCAATAGCCAGTAGGGTATGAA 426

RESULT 8
 US 10-434-665-1582
 ; Sequence 1582, Application US/10434665
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: PATH03-09
 ; CURRENT APPLICATION NUMBER: US/10/434.665
 ; CURRENT FILING DATE: 2003-05-14
 ; PRIOR APPLICATION NUMBER: US 09/134,000
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 1582
 ; LENGTH: 948
 ; TYPE: DNA
 ; ORGANISM: Enterococcus faecalis
 ; US-10-434-665-1582

Query Match 38.1%; Score 350.8; DB 8; Length 948;
 Best Local Similarity 61.7%; Pred. No. 3.8e-97;
 Matches 559; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

7 AAAACAGCCTTTTATTGCTGGCTCAAGCTGCCAGPATCTAGGGATGGGACTGGGATTTC 66
 22 AAACAGCCTTTTATTGCTGGCTCAAGCTGCCAGPATCTAGGGATGGGACTGGGATTTC 81
 67 TAATGATCAGTATCCGATGTCAGAACAGATGATCGAGCGTCAAGCTGGCTGGGTAT 126
 82 TATACCCAGAAGGGATGTCGGAAACTTGTGGAGATCTAGATCATTTAGGTAT 141
 127 GATTAGCTTATCTCATACCGAAACTCAATGACCCGTATACGCA 186
 142 GAGATGGAGAACATTGTTTACTGAAATGAGCTTAAATGAAACATACGCAA 201
 187 CCAGCCATTTCTAGGACATCTGGCTGGTGTCTACGCTTGTGGCTATACGCTTGTGGCTATACG 246
 202 CCTGCTCATTTAACGTCAGTGTGCAATTACGCTTGTGGCTATACGTTTACGCA 261
 247 CCTGATGTCAGTGTGGCTGGTGTCTACGCTTGTGGCTATACGCTTGTGGCTATACG 306
 262 CCTGATGTCAGTGTGGCTGGTGTCTACGCTTGTGGCTATACGCTTGTGGCTATACG 321
 307 TTGGATTGAGATGGCTGGTGTGGCTGGCTGGCTATACGCTTGTGGCTATACG 366
 322 TTGGCTTTCAGAGCAGCTGGCTTGTGGCTCAAGGCGTCAAGGAGGAGGCA 381
 367 GCTCTCTGTCAGTGTGGACTCTGGCAAGATGGTAGCACTGCTCAATAGCCAGTAGGGTATGAA 426

Qy 127 GATTTAGGTTAATCATCGATACTGAGAACAAACTCATCAGACCCGCTATACGCAA 186
 Db 142 GAGATGGCAGAACTTGTGTTTACTGAAATGAAATGAAATGAAATGAA 201
 Qy 187 CCAGCCATTCTAGCGACTTCGGTTGTTATCTACCGTTTATTGCAAGAAAGGGCTATCG 245
 Db 202 CCTGCTTATTTAACAGTCAGTGTGCAATTACCGTCTTACGTTCAACAAAGGCTAAAG 261
 Qy 247 CCTGATATTGGTGTGGTGTCTCCTGAGAAATACTCTGCCCTTGGCAAGGGGCC 305
 Db 262 CCTGATGTCGTAGCGGTTAAAGCTTACGGCTCTTGGTGCAGGGGT 321
 Qy 307 TTGGATTTGAGATCGGTGCTTAAGCTTACGGAAATCAGGCTCTTGGTGCAGGGGT 366
 Db 322 TTGGCTTTAGAACAGTGGCTTCAAAAGGGCTCACTACGAAAGAA 381
 Qy 367 GCTCCCTGCTGACTCTGGCAGAATGGTAGCTAACATGCCAGTGGAGGTATTGAA 426
 Db 382 GCACCAAGGAAACTGGCRAAATGGTGTCTTTATGAACTCTGACCTGAAATTTGG 441
 Qy 427 GAGGCTCTGCTCAAAGCTCTGAACTTGAGCTGGTACTCCAGGAACTATAAACACT 486
 Db 4412 AAAGCCCTGCCAGAACGTCAGTCAGTGTGGCTCAGGAAATTATAACCAA 501
 Qy 487 GCACAAATCGTATTTGGGAAAGTGGTCAAGTGTGAGCTTTGCAA 546
 Db 502 CAACAAATCGTATTTGGTCAAGGCAACTTGTGCTGTGATTAAGGATGACACTTCTCAA 561
 Qy 547 GAGGAGGTGCCAAACGGCTGATTCGAGTCCTTACACGGCTCTC 605
 Db 562 GAGGCTGTGTAAGGAAATTCGGTAAATTCGGTAAATGAGGCTCTCAGCGCTG 621
 Qy 607 CTTGAGGCTGTGCTGAGCAAACTAGTGTGAAACTCTGCTGAGTTTTCAGATT 666
 Db 622 TTACAAACAGCATCAAAATAATTGGTCAGATTAGCAAAATGAACTTCAAACGATG 681
 Qy 667 ACTTGCTCCCTAGTCGGCATACTACAGAACGGCTGCTGATGCCAAAGGACATGGCTCA 726
 Db 682 CAAATTCTGTCTTATGACTAACGACTGCCAAATTATGCCCAAGGGCAATTCAAGG 741
 Qy 727 CTCTTGACCGCTCAGGTCAAGGAACCCGTTGGTTCTATGAAAGATTGGGTATGCAA 786
 Db 742 TTATTGGAAAAGCAACSTCATCTGGGTACGGTTGAGACAGTATGCCAAACGATGAA 801
 Qy 787 GAGGAGGCAATAAGCAACTTATGAGATGGTGGAGGAAACTTGTGAGTTTGT 845
 Db 802 GCTATGAGCTAGGAGGATATTGAGTTGAGTTGCTCAGTTACTGGTTTGT 861
 Qy 847 AAAAATTTGATCAAACTGCTCACTAGTCATGTCGAAGATCAAGGGACTTTAGTACCA 905
 Db 862 AAAAATGACAAATGAAATGACCTGTTGGAGATGTGCAATACAGAA 921
 Qy 907 CTTTTA 912
 Db 922 ACGTTA 927

RESULT 9
 US-10-282-122A-21491
 Sequence 21491: Application US/10282122A
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangau
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hasebeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.

APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: EIJTRA_034A
 CURRENT APPLICATION NUMBER: US/10/282-122A
 CURRENT FILING DATE: 2003-02-20
 PRIORITY NUMBER: 60/191,078
 PRIORITY FILING DATE: 2000-03-21
 PRIORITY APPLICATION NUMBER: 60/206,848
 PRIORITY FILING DATE: 2000-05-23
 PRIORITY APPLICATION NUMBER: 60/207,727
 PRIORITY FILING DATE: 2000-05-25
 PRIORITY APPLICATION NUMBER: 60/230,335
 PRIORITY FILING DATE: 2000-09-05
 PRIORITY APPLICATION NUMBER: 60/230,347
 PRIORITY FILING DATE: 2000-09-09
 PRIORITY APPLICATION NUMBER: 60/242,578
 PRIORITY FILING DATE: 2000-10-23
 PRIORITY APPLICATION NUMBER: 60/253,625
 PRIORITY FILING DATE: 2000-11-27
 PRIORITY APPLICATION NUMBER: 60/257,931
 PRIORITY FILING DATE: 2000-12-22
 PRIORITY APPLICATION NUMBER: 60/267,636
 PRIORITY FILING DATE: 2001-02-03
 PRIORITY APPLICATION NUMBER: 60/269,308
 PRIORITY FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 21491
 LENGTH: 915
 TYPE: DNA
 ORGANISM: Enterococcus faecium
 US-10-282-122A-21491
 Query Match 34.4% ; Score 316.8 ; DB 9 ; Length 915 ;
 Best Local Similarity 60.0% ; Pred. No. 1..1e-86 ;
 Matches 547 ; Conservative 0 ; Mismatches 362 ; Indels 3 ; Gaps 1 ;
 Query 7 AAAACAGGCTTTTATTTGCTGGTCAGGTGGCCAGTATCTAGGGTGTGGACGGGTTTC 66
 Db 4 AAAACAGGCTTTTATTTGCTGGCCAGGTTGGTGTGGAAAGGTTAAAGGTTAA 63
 Query 67 TATGATCAGTATCGATTGTAAGAAACGATTGATGAGCCGATGAGTTGCTGGTTAT 126
 Db 64 TATGAAAGAG--CCGTTGAAAGGACACTTGATGAGCAAGTGTGATTCGGCTAC 120
 127 GATTACGTTTATCTCATGATACGGAAAGCAAACTCATCAGCCCGCTATAGCAA 186
 Db 128 GATATGGTGACTTGTGCTTACAGAAAATGAGCTTATGAGCTTATAGAA 180
 Query 187 CCAGCCTTCTAGCAGTCTGCTGTTGCTATCTACCGTTTATGCAAGAAAAGGGCTATCAG 246
 Db 181 CCAGCTATCTACGTOACGTCGCTTATGAGCTTATGAGCTTATGAAAGGAGCATGAAATCATC 240
 Query 247 CCTGATATGGTTGAGATGGCTGTTGCTCTGGAGAAATCTCTGCTGGCTTGTGCTTATGAGAGCT 306
 Db 241 CCAGATGCGAGCTTGTGAGTAACTGAGTTAGGAGATATTCGGATTACTAGTGTAGTATGCG 300
 Query 307 TGGGATTTGAGATGGCTGCTGCTGCTGAGCTTATGAAAGGCTTATATGAAAGGAGCG 366
 Db 301 CTATCCTTCACTGAGGAGTGGCTGCTGCTGAGCTTATGAGAGCTTATGAGAGCT 360
 Query 367 GCTCCCTGTCAGCTGCGAAAGTGGTAGCAGTCTGAACTGAGCTATGAA 426
 Db 361 GCCCCAGCTGGAAAGGGAAAATGGTGCAGTGTGATTAATGCGCTGAGTGGAG 420
 Query 427 GAGGCTCTCAAAGGCTTCTGAACTGGAGTCTACTCCAGGAAACTATACACCT 486
 Db 421 GAGGCTCTCATGAGTGGCTAGTACGTCATGTCATCTCTGCAATTATGATACCT 480
 Query 487 GCACAAATCGTCACTGGAGGAAAGCTGGTGTGAGCTTGTGAACTTTGCAA 546
 Db 481 CAGGAGATCGTCACTGGAGGAAAGCTGGTGTGAGCTTGTGAACTTTGCAA 540

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE: Enterococcus faecium

FEATURE: misc feature

NAME/KEY: (B) LOCATION 1..987

SEQUENCE DESCRIPTION: SEQ ID NO: 3319:

US-10-417-884-3319

Query Match 34.2%; Score 315.2; DB 8; Length 987;

Best Local Similarity 59.9%; Pwd. No. 3.7e-86;

Matches 546; Conservative 0; Mismatches 363; Indels 3; Gaps 1;

Qy 7 AAAACGGCTTTTATTTTCTGGCTCAGGTGCCAATATCAGGATGGGAACTTC 66

Db 73 AAAACGATCTTATTAGTGCACAAATCAAGTATGGAAAGATTCTGGCT 66

Qy 67 TATATCAGTATCGGATGTCAGGATGTCAGGTGCTGGTTAT 126

Db 133 TATAGAGAG---CCGTGTTAAAGCAGACATTGAGGAGACTGAGATTCTGGCTAC 189

Qy 127 GATTACGTATCTCATCGATAAGAACACTCAATAGACCGTATAACGAA 186

Db 190 GATGGGTGAACTTGTCTTACAGAAATGAGCAGCTTAAACAGACATTGATGAA 249

Qy 187 CCAGCATTCTAGGACTCGGTATCTACCGTTATGGAAAGAAAGGCTATAG 246

Db 250 CGAGTATCTAACGTGACTCGGTATTATCGTTATGGAAATGGAAATCATC 309

Qy 247 CCTGATATGGTGTGTTGCTCTGGAGATACTCTGCTGTTGAACTGGGCC 306

Db 310 CGATGCGGCTTCTAGGTGACTGTTAGGTGAGTGGATGAGATGGCTATGCG 369

Qy 307 TTGGATTGAAAGATGGTTGCTCTGGTAGCTAAAGGGCCATATGGAAAGACG 366

Db 370 CTATCTTCTACTGAAAGCAGTGTCTAGTAGCAAAAGGGCCTATATGAGAAGT 429

Qy 367 GCTCTGCTGACTCTGGAAAGGGTACAGTCTCATACGCGACTGAGGTCTGAA 426

Db 430 ACCCAAGTGGAAAGGGAAATGTTGAGTGTGAGTGTGAGTGTGAGATGGCTA 426

Qy 427 GAAGCCTGCAAAAGGCTCTGAACTTGGAGTGTACTCCAGCAACTATAACACCT 486

Db 490 GAACCTGCTCATGAGGCPAGCAACTACGGCATGATGAGTGTGAGTGTGAG 489

Qy 487 GCACAAATGCTCATGCTGAGAGTGTGAGTGTGAGTGTGACTTTGAA 546

Db 550 CAGCGATGCTGTTGGGGAGAAAAGCGTAGAGGAAGCTGTTTACTTAAAAA 609

Qy 547 GAAGCAGGTGCCAAAGGCTGTTGATCTCTTAAGGTGCTGGCTTACACCGCTC 606

Db 610 GAAAAGGGTCAAGAATGAGTCCTTAAGTCAGGGCTTTTATCAGGTT 669

Qy 607 CTTGAGCCCTGCTACGCCGAAACTAGCTGAAACTCTAGCTGAGTTTCAGATT 666

Db 670 TTAGACCGCAGAAAAAACCTGGGAGACCTAAGTCAGTTCAATTCTGAACT 729

Qy 667 ACTTCCTCCCTAGGGCAATACGAACTGCTGAGTATGGGTCTATGGTCAAG 726

Db 730 TCTTTCTCATCAAGGACACACAAAGGAAATATGAAAGAACAACTGCGGA 789

Qy 727 CTCTGACGGCTGAGTCAGGAACCCGTTCTGTTCTATGAGTATGGGTCTATGGAA 786

Db 790 CTACTGAAAGCAAGTGCATGCACCTGTTCTATGAGTATGGTAAAGTAAA 849

Qy 787 GAAGGGGATAAAACAACTTATGAGATTGGACGGGAAACTCTCTGTTCTGTT 846

Db 850 ACATGGGATCGAACAGTCATGAAAGTGGGCCGAAAAGTAAAGGGATTTATG 909

Qy 847 AAAAATTGATCAAATGCTCACTAGTCAGTCAAGGGAGATAAGCGAGTTAGTAGCA 906

STRANDEDNESS: double

TOPOLOGY: circular

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/417-884

FILING DATE: 17-Apr-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107-532A

FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/085,598

FILING DATE: 14-May-1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Denise

REGISTRATION NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 891-5007

TELEFAX: (781) 893-8277

INFORMATION FOR SEQ ID NO: 3319:

SEQUENCE CHARACTERISTICS:

LENGTH: 987 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

RESULTS 1.0

US-10-417-884-3319

Sequence 3319, Application US/10417884

GENERAL INFORMATION:

APPLICANT: Lynn A. Doucette-Steamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO NUMBER OF SEQUENCES: 7110

ENTEROBACTER FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 024354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/417-884

FILING DATE: 17-Apr-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107-532A

FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/085,598

FILING DATE: 14-May-1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Denise

REGISTRATION NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 891-5007

TELEFAX: (781) 893-8277

INFORMATION FOR SEQ ID NO: 3319:

SEQUENCE CHARACTERISTICS:

LENGTH: 987 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

Db 910 AAAAATCGATAAACATACCAAGTCTGGTGTGAAATAAGCAGACATTGATGAA 969
 Qy 907 CTTTGTAGAAAA 918
 Db 970 ACAATGCAATA 981

RESULT 11
 US-282-122A-41191
 GENERAL INFORMATION:
 Sequence 41191, Application US/10282122A
 APPLICANT: Wang, Liangs
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hasebeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: BLTRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-03
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 41191
 TYPE: DNA
 ORGANISM: Vibrio cholerae
 US-10-282-122A-41191

Query Match 23.5%; Score 217.6; DB 9; Length 939;
 Best Local Similarity 55.5%; Pred. No. 4.3e-56;
 Matches 484; Conservative 0; Mismatches 379; Indels 9; Gaps 3;

Qy 1 ATGACTAAACAGCCATTATGGTGTAAACARAATTCGGCTGAGCTCAGAAGTGC 135
 Db 16 ATGAGTAAGTTGGTGTATCGTATTCAGTCAGGGCTCGAAGAGTGGTATCTGGCT 75
 Qy 61 GATTCTATGATCAGTATCCGATTCGAAAGAACGATGATCGAGGAGTCACGTGCTC 120
 Db 76 GACCTTGGCAGGAGTATGCTGTGTAACAGATTCGGCTGAGCTCAGAAGTGC 177
 Qy 121 GGTATGATTTACGTTATCTCATC---GATACTGGAAAGAACGACAACTCAATCGACCGC 195
 Db 136 GTTACATCTTCGGCTGGCTGAGTCAGTCACCAACACTTC 195
 Qy 178 TATACGCAACGCCATTCTAGCAGCTTCGGTGTATCTACCGTTATGCAAGAAAG 237

RESULT 12
 US-10-282-122A-32186
 Sequence 32186, Application US/10282122A
 GENERAL INFORMATION:
 APPLICANT: Ward, Liangs
 APPLICANT: Zamudio, Carlos
 APPLICANT: Hasebeck, Robert
 APPLICANT: Malone, Cheryl
 APPLICANT: Ohlsen, Kari
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: BLTRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 41191
 LENGTH: 939
 TYPE: DNA
 ORGANISM: Vibrio cholerae
 US-10-282-122A-41191

Query Match 23.5%; Score 217.6; DB 9; Length 939;
 Best Local Similarity 55.5%; Pred. No. 4.3e-56;
 Matches 484; Conservative 0; Mismatches 379; Indels 9; Gaps 3;

Qy 1 ATGACTAAACAGCCATTATGGTGTAAACARAATTCGGCTGAGCTCAGAAGTGC 135
 Db 16 ATGAGTAAGTTGGTGTATCGTATTCAGTCAGGGCTCGAAGAGTGGTATCTGGCT 75
 Qy 61 GATTCTATGATCAGTATCCGATTCGAAAGAACGATGATCGAGGAGTCACGTGCTC 120
 Db 76 GACCTTGGCAGGAGTATGCTGTGTAACAGATTCGGCTGAGCTCAGAAGTGC 177
 Qy 121 GGTATGATTTACGTTATCTCATC---GATACTGGAAAGAACGACAACTCAATCGACCGC 195
 Db 136 GTTACATCTTCGGCTGGCTGAGTCAGTCACCAACACTTC 195
 Qy 178 TATACGCAACGCCATTCTAGCAGCTTCGGTGTATCTACCGTTATGCAAGAAAG 237

PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-22
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 32186
 LENGTH: 930
 TYPE: DNA
 ORGANISM: Proteus mirabilis
 US-10-282-122A-32186

Query Match 21.3% ; Score 196.4 ; DB 9 ; Length 930 ;
 Best Local Similarity 53.0% ; Pred. No. 1.5e-49 ;
 Matches 491 ; Conservative 0 ; Mismatches 426 ; Indels 9 ; Gaps 3 ;

Qy 1 ATGACTAAACAGCCTTTTATTGCGTCAGGCCAGTATGGATGGACGG 60
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 Qy 61 GATTCTATGATCAGTATCGATTGTGCAAGAAACGATGTGCGAGTC 120
 Db 61 GAACTTGCGGAGGATTAATCCAAATAGTGCAAGAACATTGCTCAAGCATGTATG 120
 Qy 121 GGTATGATTTAGTTATCTCATGATAAGGAA--GAAGACAAATCTACAGGCCG 177
 Db 121 GGTATTTCTTGGATTAGTGCAAAATGCTGAGAGGTTAACAAACATGG 180
 Qy 178 TATAGGCAACCGCCATTCTAGGACTCTGGTGTATCTACCGTTATTCGAAAA-- 235
 Db 181 AAAACAGCAGCCGCAATTACGAGATCCGTTGCTATTCGCAAGAAAAA 240
 Qy 236 -AGGGCTATCAGCTGATATGTTGCTGCTGTGCTGAGAAATACTCTGCCTTGGTG 294
 Db 241 CAAAGGCAAAATGCCAACATGATGGCAGGTACAGTCTGTGATCTGCTTGTAC 300
 Qy 295 GCAAGGCCGCGCTTGGATTTCAGATGGCTGCGTTGAGCTTGGAGCTAT 354
 Db 301 TGTGCTGGTAAATGATTGTTCTGGGGATAAACTAGTAAATGGGGTAAATA 360
 Qy 355 ATGGAAAGGGCTCTGGTCACTCTGGCAAGATGGTAGGAGTCTCAAATAGCCAGTA 414
 Db 361 ATGCAAGGGCTGTTGCTGACTCTGGCCATATGGAAATTATGGTATTGAAAT 420
 Qy 415 GAGGTCTATGAGAAGGCTGCAAAAGCTCTGACTGGAGTTACTCCGCCAAC 474
 Db 421 GATGCTATGCAAAAGTGTGAAAGTGGCAGTGTCTACCTGTGAC 480
 Qy 475 TATAACACCTGCAAAATCTGTTGAGTGGCTGAACTTGGTGTGAGCTT 534
 Db 481 TTAACTACCGGTCAAGTGGTGTGAGCTTGGCTGAACTTGGTGTGAGCTT 540
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 Db 541 GATTATGTTAAAGAAGCTGGACAAAGTGGTGTGAGCTTGGTGTGAGCTT 600
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 Qy 661 TTAAACACCTGCAAACTGTTGAGTGGCTGAACTTGGTGTGAGCTTGGTGTGAGCTT 720

RESULT 3
 US-10-282-122A-21907
 ; Sequence 21907, Application US/10282-122A
 ; GENERAL INFORMATION:
 / APPLICANT: Wang, Liangsu
 / APPLICANT: Zamudio, Carlos
 / APPLICANT: Malone, Cheryl
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Chien, Kari
 / APPLICANT: Zyskind, Judith
 / APPLICANT: Wall, Daniel
 / APPLICANT: Travick, John
 / APPLICANT: Carr, Grant
 / APPLICANT: Yamamoto, Robert
 / APPLICANT: Forzych, R.
 / APPLICANT: Xu, H.
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 / FILE REFERENCE: ELITRA.034A
 / CURRENT APPLICATION NUMBER: US/10/282-122A
 / CURRENT FILING DATE: 2003-02-20
 / PRIOR APPLICATION NUMBER: 60/191,078
 / PRIOR FILING DATE: 2000-03-21
 / PRIOR APPLICATION NUMBER: 60/206,848
 / PRIOR FILING DATE: 2000-05-23
 / PRIOR APPLICATION NUMBER: 60/207,727
 / PRIOR FILING DATE: 2000-05-26
 / PRIOR APPLICATION NUMBER: 60/230,335
 / PRIOR FILING DATE: 2000-09-06
 / PRIOR APPLICATION NUMBER: 60/230,347
 / PRIOR FILING DATE: 2000-09-09
 / PRIOR APPLICATION NUMBER: 60/242,578
 / PRIOR FILING DATE: 2000-10-23
 / PRIOR APPLICATION NUMBER: 60/253,625
 / PRIOR FILING DATE: 2000-11-27
 / PRIOR APPLICATION NUMBER: 60/257,931
 / PRIOR FILING DATE: 2000-12-22
 / PRIOR APPLICATION NUMBER: 60/267,636
 / PRIOR FILING DATE: 2001-02-09
 / PRIOR APPLICATION NUMBER: 60/269,308
 / PRIOR FILING DATE: 2001-02-16
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 78614
 / SEQ ID NO: 21907
 / SOFTWARE: PatentIn version 3.1
 / LENGTH: 939
 / TYPE: DNA
 / ORGANISM: Haemophilus influenzae
 US-10-282-122A-21907

Query Match 21.3% ; Score 196.4 ; DB 9 ; Length 939 ;
 Best Local Similarity 54.1% ; Pred. No. 1.5e-49 ;
 Matches 470 ; Conservative 0 ; Mismatches 386 ; Indels 12 ; Gaps 3 ;

1 ATGCTAAACAGCTTTTATTCGATGTCAGTGCCGATATTAGGATGGACGG 60
 1 ATGAAATTGGAATGCTTCCAGTCAGGTCAGCTGATGCTGCT 60
 61 GATTCTATGATCGTATCCGATTGCAAGAACGATTGATGAGGAGTCGCTC 120
 61 GATTGAACTGATACTCAAATGATTGAACTTAAAGGATGATGCGCT 120
 121 GGATGATTAGTTACGTTATCTCATGATACGG - - AAGAAGAACAACTCAATCAACAGCCGC 177
 121 GGATGATTATGATGATGATGTTGTCAGGTCAGCTGAACTTAATACTGG 180
 178 TATPGGCAACCAGCAGCTCTAGGGACTCGGGCTATCTACCGTTATTGCAAAAG 237
 181 CAAACTGACCCGGACATTAGCTGCTCACTGCTGCTATTATCGGTATGAAAGAAA 240
 238 GGCTATC - - - AGCCCTGATATGGCTGCTGCTCTGGAGATACTCTGCTTG 291
 241 TTCTCTCAATTAAACCGAAAGTGTGGAGCTCATGCTTAGGTGTTATCTGGTT 300
 292 GTGGCAAGGGGCCCTGGATTTGAGATGGCTTGCTTGAGTAACGGTGAGGCC 351
 301 GTTGTGCTGGCTGTTGGATTCAAGTCAGTCATGCAATTAAATTGGGATTGCGGAAA 360
 352 TATGGGAAAGGGGCTCTGCTGACTCTGGCAAGATGGTGCAGTCTCAATAGCCA 411
 361 TTATGCAAACTGGCTGAACTGGCTGATGCTGAACTATGGTTAGAT 420
 412 GTAGGGCATTTGAGAACGCTGTCAAAAGCTTGTAACTGGAGGTTACTCAGCC 471
 421 AATGGCAATTAAATTAATCTGGCAAAATGGCTGAGTGGCTGATCTGGCT 480
 472 AACPTAAACACTGACAATGCTCATGGAGAGTGTGAGTGTGAGAGG 531
 481 AACATTAACTCACGGGTCAAGPAGTTATGGGGTGGAAAGCTGAGCTGCG 540
 532 GTTGACTTTGGAGAACGGGCCAACTGGCTTGTAACTGGAGGTTACTCAGCC 591
 541 GTCGATATTGTAAGAACGGGGGAAACGTCATGGCTTGTGAGCTGACCT 600
 592 TTTACACGGCTCTCTGACGGCTGCTAGCCAGAAACTCTAGCTCAGGT- 650
 601 TCTACTGTGCAATTGAAACTTAGCGTAAACTTAGGATT 660
 651 -AGTTTTCAGTTTACTGTCCCTAGTGGCAATACAGAACGCTGCTGATGCAA 708
 661 CAAPTTAAACACAAATACTGGTATAAAATACTGGTAAAGCTGAAACTGAA 720
 709 AAAAGGAAATTGGCTGAGCTCTAACGGCTGAGTGGCTGAGTGGCTGAA 768
 721 GGCCCCGAAATTCTACGGCACTGTGGCTGCTGTATAATAGTCAGTGTGGACTGAA 780
 769 AGTATTGGGCTCATGCAAAAGGGCATAAGGAACTTATGGACGGCAA 828
 781 ACATTTGAAATTGGCGAAGTGGCTTGTGCTAGTGGCTGAAAGTGGCGAGGTAA 840
 829 GTCTGTGCAAGGTTGTTAAAAAATTG 856
 841 GTATTAATGGTTAACCAAACGGATTG 868

RESULT 14
 US-08-487-429B-1/C
 Sequence 1, Application US/08487429B
 GENERAL INFORMATION:
 APPLICANT: Fleischmann et al.
 TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
 CURRENT APPLICATION NUMBER: P8186P1
 CURRENT FILING DATE: 1995-04-07
 PRIOR APPLICATION NUMBER: US 08/426,787
 PRIORITY FILING DATE: 1995-04-07
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
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 LENGTH: 1830121
 TYPE: DNA
 ORGANISM: Haemophilus influenzae
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Query Match 21.3% Score 196.4; DB 4; Length 1830121;
Best Local Similarity 54.1%; Pred. No. 3.9e-18;
Matches 470; Conservative 0; Mismatches 386; Indels 12; Gaps 3;

QY 1 ATGACTAAACAGCCCTTTTATTGCTGGTCAAGGTCCCACATCTAGGGATGGACGG 60
Db 172507 ATGAAAAATTCCCAATGGTCTCCAGTCAGGTCCAAACTGCGTATGCT 172448

QY 61 GATTCTATGATACTGATTCGATTGTAAGAAACATTGATCAGCGAGTCAGGTCTC 120
Db 172447 GATTCTGAACTGATAATCCATTGAACTTAAACAGATCTGATGGCTT 172388

QY 121 GGTATGATTAGTTATCTCATGATACTGAACTCATGACGCC 177
Db 172387 GGTTATGATTATGGTATCTGGTCACAAGTCACCTGAACTTAATAACCTGG 172328

QY 178 TATAGCACCAGCCATTAGGCACCTGGGACTCGGTGCTTACCGTTTATGCAAGAAAG 237
Db 172327 CAAACTCGGCCCACTTATGCTCATGCTTACGTCATTATCGCTATGGAAAGAAA 172266

QY 238 GGATTC-----AGCTTGATATGGTGGTGTCTGGATCTGGAACTCTGGTTG 291
Db 172267 TTTCCTCAATTAAAACCAAGACTGATGGCAGTCATAGCTTGGTGAATCTGGTTA 172208

QY 292 GTGGCAAGGGGCGCTTGGATTGGACATGGGTGCCTTGGTAGTAAGGTGGAGCC 351
Db 172207 GTTGTGCTGGCTGTTGGATTTGGAAATTGGGAAATTGGGAAAT 172148

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Qy 352 TATATGGAAAGAGGGCTCCCTGCTGACTCTGGCAAGATGGTAGGTTCTCAATAGGCCA 411
 Db 172147 TTAATGCAACAGCTGTGCTGAAGCATACTGGCAATCTGGTTAGT 172088
 Qy 412 GTAGAGGTATTGAAAGGCTGTCAAAGCTCTGAAATTGAGTTACTCCAGGC 471
 Db 172087 AATGAGCAATTAAATGCTTGAAACAGCAGGAAAGTGGTATCTGGCTG 172028
 Qy 472 AACTATAACACCTGCAACATGTCATGCTGGAAAGTGGTGCAGTTGATCGAGG 531
 Db 172027 AACTTAACATACGGTCAAGTAGTTATCGGGTCAAAGGTGAGTTGAGG 171968
 Qy 532 GTTGAACTTTGCAAAAGCAGGTGCAACGCTGTATCCTTAAGGTGAGGTCC 591
 Db 171967 GCTGCAATTGTAAGGAGGGAAACGCTGATGGCTAGTGTGAGGTACT 171908
 Qy 592 TTTACACCGCTCTCTTGAACGAGGTGCTGTAGCCAAACTAGTCAGGT 650
 Db 171907 TCTCATGTGATTAAATGAACTGGGAGGATACGGTAACTTGAGAAATT 171848
 Qy 651 -AAGTTTCAGATTACTGTCCCTAGTCAGAAAGCTGTGATGAA 708
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 Db 171787 GGCACCGAAATTCTGACCGACTTGCGTCAGTTATAGTCAGTTGGACTGA 171728
 Qy 769 ATGATGGGGTATGAAAGGAGGCACTTATGCACTTATAGTCAGTTGGACTGA 828
 Db 171727 ACAGTGAAAAATGGCCAGATGGCTCTAGTGCTGAGTTGGCAGGTAA 171666
 Qy 829 GTCCTGTCAGTTTTTAAATGG 856
 Db 171667 GTTAAATGGTTAACAAACGCAFTG 171640

RESULT 15
 *US-10-329-960-1/c
 Sequence 1, Application US/10329960
 GENERAL INFORMATION:
 APPLICANT: Fleischmann et al.
 TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
 FILE REFERENCE: P1186P1
 CURRENT APPLICATION NUMBER: US/10/329,960
 CURRENT FILING DATE: 2003-01-02
 PRIOR APPLICATION NUMBER: US 09/643,990
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: US 08/487,429
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: US 08/426,787
 PRIOR FILING DATE: 1995-04-21
 NUMBER OF SEQ ID NOS: 1
 LENGTH: 1830121
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 1
 TYPE: DNA
 ORGANISM: Haemophilus influenzae

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LOCATION: (145171) .. (145171)

Qy	709	AAAGAGGACATTGGCTAGCTCTTGAAGCTAGGTCAGGAAACCGTTCTATGAA	768
Db	171787	GCCACCCAAATTCTGTAACGCCACTTGTGGCTAGTATAAGTCAGTTGTGGACTGAA	171728
Qy	769	AGTATGGGCTATGAAAGCAGGCTATAGCAACTTATCGAGATTGACCGGGAA	828
Db	171727	ACAGTCAAAATGGCAGATGCGTCTAGGCTCTAGTCAGTGGCCAGGTAAA	171668
Qy	829	GTCCTGTCAGGTTTGTAAATTTG	856
Db	171667	GTATTAATGGTTAACCAACGCTTG	171640

Search completed: June 11, 2003, 19:58:48
Job time : 707 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 11, 2003, 20:02:58 ; Search time 233 Seconds

(without alignments) 846.731 Million cell updates/sec

Title: US-09-308-397-2

Perfect score: 1518

Sequence: 1 MTKTAFILFAGQGAQYLGGMGR.....QTAHLAHVEDQASLVALLEK 306

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing First 45 summaries

Database : Pending Patents AA Main: *

1: /cgn2_6/ptodata/7/paa/1/CTUS_COMB_pep:*

2: /cgn2_6/ptodata/2/paa/US06_COMB_pep:*

3: /cgn2_6/ptodata/2/paa/US07_COMB_pep:*

4: /cgn2_6/ptodata/2/paa/US08_COMB_pep:*

5: /cgn2_6/ptodata/2/paa/US08_1_COMB_pep:*

6: /cgn2_6/ptodata/2/paa/US082_COMB_pep:*

7: /cgn2_6/ptodata/2/paa/US083_COMB_pep:*

8: /cgn2_6/ptodata/2/paa/US084_COMB_pep:*

9: /cgn2_6/ptodata/2/paa/US085_COMB_pep:*

10: /cgn2_6/ptodata/2/paa/US086_COMB_pep:*

11: /cgn2_6/ptodata/2/paa/US087_COMB_pep:*

12: /cgn2_6/ptodata/2/paa/US088_COMB_pep:*

13: /cgn2_6/ptodata/2/paa/US089_COMB_pep:*

14: /cgn2_6/ptodata/2/paa/US090_COMB_pep:*

15: /cgn2_6/ptodata/2/paa/US091_COMB_pep:*

16: /cgn2_6/ptodata/2/paa/US092_COMB_pep:*

17: /cgn2_6/ptodata/2/paa/US093_COMB_pep:*

18: /cgn2_6/ptodata/2/paa/US094_COMB_pep:*

19: /cgn2_6/ptodata/2/paa/US095_COMB_pep:*

20: /cgn2_6/ptodata/2/paa/US096_COMB_pep:*

21: /cgn2_6/ptodata/2/paa/US097_COMB_pep:*

22: /cgn2_6/ptodata/2/paa/US098_COMB_pep:*

23: /cgn2_6/ptodata/2/paa/US099_COMB_pep:*

24: /cgn2_6/ptodata/2/paa/US100_COMB_pep:*

25: /cgn2_6/ptodata/2/paa/US101_COMB_pep:*

26: /cgn2_6/ptodata/2/paa/US102_COMB_pep:*

27: /cgn2_6/ptodata/2/paa/US60_COMB_pep:*

7 1514 99.7 306 22 PCT-US02-03987-13580
 8 1514 99.7 306 24 US-09-815-242-13580
 9 1514 99.7 306 24 Sequence 13580, A
 10 1048 69.0 308 15 Sequence 13580, A
 11 948 62.5 328 15 Sequence 13580, A
 12 948 62.5 328 15 Sequence 13580, A
 13 937 61.7 313 1 Sequence 13580, A
 14 937 61.7 313 22 Sequence 13580, A
 15 937 61.7 313 24 Sequence 13580, A
 16 937 61.7 313 15 Sequence 13580, A
 17 863 56.9 182 17 Sequence 6, Appli
 18 670 44.1 137 12 Sequence 407, App
 19 669.5 44.1 317 21 Sequence 62681, A
 20 669.5 44.1 317 27 Sequence 23122, A
 21 654 43.1 313 19 Sequence 7983, A
 22 641.5 42.7 333 19 Sequence 7983, A
 23 646 42.6 306 27 Sequence 19114, A
 24 646 42.6 313 23 Sequence 14562, A
 25 643.5 42.4 309 21 Sequence 10125, A
 26 643.5 42.4 309 22 Sequence 10125, A
 27 643.5 42.4 309 24 Sequence 10125, A
 28 643.5 42.4 309 24 Sequence 10125, A
 29 633.5 42.4 309 27 Sequence 793, App
 30 636 41.9 312 21 Sequence 10975, A
 31 636 41.9 312 21 Sequence 10975, A
 32 636 41.9 312 22 Sequence 10975, A
 33 636 41.9 312 24 Sequence 10975, A
 34 632 41.6 318 21 Sequence 10975, A
 35 619 40.8 311 27 Sequence 10002, A
 36 616.5 40.6 309 21 Sequence 44244, A
 37 613 40.4 122 17 Sequence 4, Appli
 38 611.5 40.3 307 21 Sequence 12057, A
 39 594.5 39.2 326 21 Sequence 45311, A
 40 594.5 39.2 326 27 Sequence 62, Appli
 41 594.5 39.2 576775 12 Sequence 2, Appli
 42 594.5 39.2 576775 12 Sequence 2, Appli
 43 594.5 39.2 576775 18 Sequence 2, Appli
 44 594.5 39.2 576775 22 Sequence 2, Appli
 45 593 39.1 306 27 Sequence 7062, Ap

ALIGNMENTS

RESULT 1
 US-09-308-397-2
 / Sequence 2, Application US/09308397

; GENERAL INFORMATION:

; APPLICANT: Gentry, Daniel R.

; APPLICANT: Lonsdale, John T.

; APPLICANT: Payne, David J.

; APPLICANT: Pearson, Stewart C.

; APPLICANT: Van Aller, Glenn

; TITLE OF INVENTION: Novel Fabb

; FILE REFERENCE: B50593

; CURRENT APPLICATION NUMBER: US/09/308,397

; CURRENT FILING DATE: 1999-05-18

; EARLIER APPLICATION NUMBER: US 60/031,160

; EARLIER FILING DATE: 1997-11-14

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 2

; LENGTH: 306

; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae

; US-09-308-397-2

Query Match 100% Score 1518; DB 17; Length 306;
 Best Local Similarity 100%; Pred. No. 6.7e-139;
 Matches 306; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

Query

Length

DB

ID

Score

Match

Length

DB

ID

Score

Qy 1 MTKTAFLFAGQAGAQYLGNGRDFYDQPIVKETIDRASQVLGYDLRYLIDTEDKLNQTRY 60
 Db 1 MTKTAFLFAGQAGAQYLGNGRDFYDQPIVKETIDRASQVLGYDLRYLIDTEDKLNQTRY 60

Qy 61 TQPAILATSVAIRLQLQFKYQDFDMVAGSLGYSALVAGSLDFEAVALVAKRGAYME 120
 Db 61 TQPAILATSVAIRLQLQFKYQDFDMVAGSLDFEAVALVAKRGAYME 120

Qy 121 EAAPADSCKMVAVLNTPVIEFACQKQSELGYTPANNTPAQIVIAGEVYAVDRAVEL 180
 Db 121 EAAPADSCKMVAVLNTPVIEFACQKQSELGYTPANNTPAQIVIAGEVYAVDRAVEL 180

Qy 181 LQAGAKLPLKVSQPHPTALLEPASQKLASTLAQYSFSDFTCPLYGNTAAVYMQKEDI 240
 Db 181 LQAGAKLPLKVSQPHPTALLEPASQKLASTLAQYSFSDFTCPLYGNTAAVYMQKEDI 240

Qy 241 AQLTRQKEPYRFYESGVMQEGAGISMFIEGPKVLSGFVKKIDQTAHLAHVEDQASL 300
 Db 241 AQLTRQKEPYRFYESGVMQEGAGISMFIEGPKVLSGFVKKIDQTAHLAHVEDQASL 300

Qy 301 VALLEK 306
 Db 301 VALLEK 306

RESULT 2
 US-09-583-110-3912
 ; Sequence 3912, Application US/09583110

; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stumm et al.
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to *Streptococcus*
 ; FILE INVENTION: Protona for Diagnostics and Therapeutics
 ; FILE REFERENCE: PATH00-07A
 ; CURRENT APPLICATION NUMBER: US/09/583.110
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/107,433
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/085,131
 ; PRIOR FILING DATE: 1998-05-12
 ; PRIOR APPLICATION NUMBER: US 60/051,553
 ; PRIOR FILING DATE: 1998-07-02
 ; NUMBER OF SEQ ID NOS: 5322
 ; SEQ ID NO 3912
 ; LENGTH: 306
 ; TYPE: PRT
 ; ORGANISM: *Streptococcus pneumoniae*
 ; US-09-583-110-3912

Query Match 100.0%; Score 1518; DB 21; Length 306;
 Best Local Similarity 100.0%; Pred. No. 6.7e-139; Mismatches 0; Indels 0; Gaps 0;
 Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTKTAFLFAGQAGAQYLGNGRDFYDQPIVKETIDRASQVLGYDLRYLIDTEDKLNQTRY 60
 Db 1 MTKTAFLFAGQAGAQYLGNGRDFYDQPIVKETIDRASQVLGYDLRYLIDTEDKLNQTRY 60

Qy 61 TQPAILATSVAIRLQLQFKYQDFDMVAGSLDFEAVALVAKRGAYME 120
 Db 61 TQPAILATSVAIRLQLQFKYQDFDMVAGSLDFEAVALVAKRGAYME 120

Qy 121 EAAPADSCKMVAVLNTPVIEFACQKQSELGYTPANNTPAQIVIAGEVYAVDRAVEL 180
 Db 121 EAAPADSCKMVAVLNTPVIEFACQKQSELGYTPANNTPAQIVIAGEVYAVDRAVEL 180

Qy 181 LQAGAKLPLKVSQPHPTALLEPASQKLASTLAQYSFSDFTCPLYGNTAAVYMQKEDI 240
 Db 181 LQAGAKLPLKVSQPHPTALLEPASQKLASTLAQYSFSDFTCPLYGNTAAVYMQKEDI 240

Qy 241 AQLTRQKEPYRFYESGVMQEGAGISMFIEGPKVLSGFVKKIDQTAHLAHVEDQASL 300
 Db 241 AQLTRQKEPYRFYESGVMQEGAGISMFIEGPKVLSGFVKKIDQTAHLAHVEDQASL 300

Qy 301 VALLEK 306
 Db 301 VALLEK 306

RESULT 4
 US-09-583-110-3912
 ; Sequence 3912, Application US/09583110

; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stumm et al.
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to *Streptococcus*
 ; FILE INVENTION: Protona for Diagnostics and Therapeutics
 ; FILE REFERENCE: PATH00-07A
 ; CURRENT APPLICATION NUMBER: US/09/583.110
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/107,433
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/085,131
 ; PRIOR FILING DATE: 1998-05-12
 ; PRIOR APPLICATION NUMBER: US 60/051,553
 ; PRIOR FILING DATE: 1998-07-02
 ; NUMBER OF SEQ ID NOS: 5322
 ; SEQ ID NO 3912
 ; LENGTH: 306
 ; TYPE: PRT
 ; ORGANISM: *Streptococcus pneumoniae*
 ; US-09-583-110-3912

Query Match 100.0%; Score 1518; DB 21; Length 306;
 Best Local Similarity 100.0%; Pred. No. 6.7e-139; Mismatches 0; Indels 0; Gaps 0;
 Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTKTAFLFAGQAGAQYLGNGRDFYDQPIVKETIDRASQVLGYDLRYLIDTEDKLNQTRY 60
 Db 1 MTKTAFLFAGQAGAQYLGNGRDFYDQPIVKETIDRASQVLGYDLRYLIDTEDKLNQTRY 60

Qy 61 TQPAILATSVAIRLQLQFKYQDFDMVAGSLDFEAVALVAKRGAYME 120
 Db 61 TQPAILATSVAIRLQLQFKYQDFDMVAGSLDFEAVALVAKRGAYME 120

Qy 121 EAAPADSCKMVAVLNTPVIEFACQKQSELGYTPANNTPAQIVIAGEVYAVDRAVEL 180
 Db 121 EAAPADSCKMVAVLNTPVIEFACQKQSELGYTPANNTPAQIVIAGEVYAVDRAVEL 180

Qy 181 LQAGAKLPLKVSQPHPTALLEPASQKLASTLAQYSFSDFTCPLYGNTAAVYMQKEDI 240
 Db 181 LQAGAKLPLKVSQPHPTALLEPASQKLASTLAQYSFSDFTCPLYGNTAAVYMQKEDI 240

Qy 241 AQLTRQKEPYRFYESGVMQEGAGISMFIEGPKVLSGFVKKIDQTAHLAHVEDQASL 300
 Db 241 AQLTRQKEPYRFYESGVMQEGAGISMFIEGPKVLSGFVKKIDQTAHLAHVEDQASL 300

Qy 301 VALLEK 306
 Db 301 VALLEK 306

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 143
 LENGTH: 306
 TYPE: PROTEIN
 ORGANISM: *Streptococcus pneumoniae*
 US-60-174-089-143

Query Match 100.0%; Score 1518; DB 27; Length 306;
 Best Local Similarity 100.0%; Pred. No. 6.7e-139;
 Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTKTAAFLAGGAQYLGMGRDFYDQYPIVETIDRASQVLGYDRLITIDEKDKNQRY 60
 Db 1 MTKTAAFLAGGAQYLGMGRDFYDQYPIVETIDRASQVLGYDRLITIDEKDKNQRY 60

Qy 61 TQPAILATSVAYRLQEQKGYQDMVAGLSGEYSAVALSGALDFDAVALVAKRGAYME 120
 Db 61 TQPAILATSVAYRLQEQKGYQDMVAGLSGEYSAVALSGALDFDAVALVAKRGAYME 120

Qy 121 EAAPADSGKMYAVLNTPVVEACOKASELGVVTPANTPAQIVIAGSEVVAVDRAVEL 180
 Db 121 EAAPADSGKMYAVLNTPVVEACOKASELGVVTPANTPAQIVIAGSEVVAVDRAVEL 180

Qy 181 LQEAGAKRLIPLKVGSPHTALLEPASQKLAETLAQVSFSDFTCPVGNTEAAYMOKEDI 240
 Db 181 LQEAGAKRLIPLKVGSPHTALLEPASQKLAETLAQVSFSDFTCPVGNTEAAYMOKEDI 240

Qy 241 AQLITRQKEPVRYFESIGNMQEAGISNFLEIGPSKVLSSFVKKIDQTAHLAHVEDQASL 300
 Db 241 AQLITRQKEPVRYFESIGNMQEAGISNFLEIGPSKVLSSFVKKIDQTAHLAHVEDQASL 300

Qy 301 VALLEK 306
 Db 301 VALLEK 306

RESULT 5
 US-09-107-433-3397
 / Sequence 3397, Application US/09107433

GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
 SEQUENCES RELATING TO *STREPTOCOCCUS PNEUMONIAE* FOR DIAGNOSIS
 NUMBER OF SEQUENCES: 5:206

CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454

COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER SYSTEM: <Unknown>
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,433
 FILING DATE: 30-Jun-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/ 085131
 FILING DATE: MAY 12, 1998
 APPLICATION NUMBER: 60/051553
 FILING DATE: JULY 2, 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Arinello, Pamela Denene
 REGISTRATION NUMBER: 40,189
 REFERENCE/DOCKET NUMBER: GTC-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-8277
 TELEFAX: (781)893-8207

INFORMATION FOR SEQ ID NO: 3397:

SEQUENCE CHARACTERISTICS:
 LENGTH: 307 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1..307
 SEQUENCE DESCRIPTION: SEQ ID NO: 3397:
 US-09-107-433-3397

Query Match 100.0%; Score 1518; DB 15; Length 307;
 Best Local Similarity 100.0%; Pred. No. 6.8e-139;
 Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTKTAAFLAGGAQYLGMGRDFYDQYPIVETIDRASQVLGYDRLITIDEKDKNQTRY 60
 Db 2 MTKTAAFLAGGAQYLGMGRDFYDQYPIVETIDRASQVLGYDRLITIDEKDKNQTRY 61

Qy 61 TQPAILATSVAYRLQEQKGYQDMVAGLSGEYSAVALSGALDFDAVALVAKRGAYME 120
 Db 62 TQPAILATSVAYRLQEQKGYQDMVAGLSGEYSAVALSGALDFDAVALVAKRGAYME 121

Qy 121 EAAPADSGKMYAVLNTPVVEACOKASELGVVTPANTPAQIVIAGSEVVAVDRAVEL 180
 Db 122 EAAPADSGKMYAVLNTPVVEACOKASELGVVTPANTPAQIVIAGSEVVAVDRAVEL 181

Qy 181 LQEAGAKRLIPLKVGSPHTALLEPASQKLAETLAQVSFSDFTCPVGNTEAAYMOKEDI 240
 Db 182 LQEAGAKRLIPLKVGSPHTALLEPASQKLAETLAQVSFSDFTCPVGNTEAAYMOKEDI 241

Qy 241 AQLITRQKEPVRYFESIGNMQEAGISNFLEIGPSKVLSSFVKKIDQTAHLAHVEDQASL 300
 Db 242 AQLITRQKEPVRYFESIGNMQEAGISNFLEIGPSKVLSSFVKKIDQTAHLAHVEDQASL 301

RESULT 6
 PC7-US9-22578-171
 / Sequence 171, Application PC/TUS9722578
 ; GENERAL INFORMATION:
 / APPLICANT: Baitz, Richard H.
 / APPLICANT: Burnett, Stanley G.
 / APPLICANT: Dehoff, Bradley S.
 / APPLICANT: Jaskunas Jr., Stanley R.
 / APPLICANT: Mills, Bradley J.
 / APPLICANT: Morris, Franklin H.
 / APPLICANT: Peery, Robert B.
 / APPLICANT: Rostock Jr., Paul R.
 / APPLICANT: Skatrud, Paul L.
 / APPLICANT: Smith, Michele C.
 / APPLICANT: Rockey, Pamela K.
 / APPLICANT: Young-Bellido, Michele
 TITLE OF INVENTION: *Streptococcus pneumoniae* DNA Sequences
 NUMBER OF SEQUENCES: 228
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Eli Lilly and Company
 STREET: Lilly Corporate Center
 CITY: Indianapolis
 STATE: Indiana
 COUNTRY: U.S.
 ZIP: 46285
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/22578
FILING DATE:

CLASSIFICATION:
NAME: Webster, Thomas D.

REGISTRATION NUMBER: 39 872
REFERENCE/DOCKET NUMBER: X-11162

TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334

INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids

TYPE: amino acid
STRANDEDNESS: Not Relevant

TOPOLOGY: Peptide
MOLECULE TYPE: Peptide

HOMOTHECTICAL: NO
ANTI-SENSE: NO

PCT/US97-22578-171

Query Match
Best Local Similarity 99.8%; Score 1515; DB 1; Length 306;

Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 301 VALIEK 306

RESULT 8
US-09-815-242-13580

Sequence 13580, Application US/09815242

GENERAL INFORMATION:

APPLICANT: Hasebeck, Robert

APPLICANT: Olsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trwick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.01A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14,110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13580

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-09-815-242-13580

Query Match
Best Local Similarity 99.7%; Score 1514; DB 1; Length 306;
Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
PCT-US02-03987-13580

Query Match
Best Local Similarity 99.7%; Score 1514; DB 1; Length 306;
Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
PCT-US02-03987-13580

Qy 61 TQPAIILATSVAYRLLQEQKQYQDMVAGSILGEYSAVVALGALDFEDAVALVAKGAYME 120
 Db 61 TQPAIILATSVAYRLLQEQKQYQDMVAGSILGEYSAVVALGALDFEDAVALVAKGAYME 120
 Qy 121 EAAPADSGKMYAVLNTPVEVIEAACQASELGVUTPANTNTPAQIVIAGEVVAVDRAVEL 180
 Db 121 EAAPADSGKMYAVLNTPVEVIEAACQASELGVUTPANTNTPAQIVIAGEVVAVDRAVEL 180
 Qy 181 LQEAGAKRKLPILKVSQSPHTALLEPASQKLAETLAQVSFSDETCFLVGNTEAAVMQKEDI 240
 Db 181 LQEAGAKRKLPILKVSQSPHTALLEPASQKLAETLAQVSFSDETCFLVGNTEAAVMQKEDI 240
 RESULT 10
 US-60-160-039-18370
 Qy 241 AQLITRQKEPVRFYESIGVMOEAGISNFIEIGPGKVLSGPVKIKIDQTAHLAHVEDQASL 300
 Db 241 AQLITRQKEPVRFYESIGVMOEAGISNFIEIGPGKVLSGPVKIKIDQTAHLAHVEDQASL 300
 ; GENERAL INFORMATION:
 ; Sequence 18370, Application US/60360039
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldmat, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-101520521A
 ; CURRENT APPLICATION NUMBER: US/60/360, 039
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO: 18370
 ; LENGTH: 308
 ; TYPE: PRT
 ; ORGANISM: Lactococcus lactis
 US-60-160-039-18370

Query Match 69.0% ; Score 1048; DB 27; Length 308;
 Best Local Similarity 67.5%; Pred. No. 5.1e-03;
 Matches 208; Conservative 40; Mismatches 58; Indels 2; Gaps 1;

Qy 1 MTKTAFLFAGGQQAQYLGMRDFYDQPIVKETIDRASQVLGQYDILRMLIDTBEDKLNQTRY 60
 Db 1 MTKTAFLFSGQQAQKLMARDLYDQETVKATFDEASQALGYDILRLLIDTBEDKLNQTRY 60
 ; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
 ; FILE REFERENCE: ELITRA-028A
 ; CURRENT APPLICATION NUMBER: US/10/072, 851
 ; CURRENT FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: 60/267, 636
 ; PRIOR FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 1581
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 13580
 ; LENGTH: 306
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-10-072-851-13580

Query Match 99.7% ; Score 1514; DB 24; Length 306;
 Best Local Similarity 99.7%; Pred. No. 1.7e-138;
 Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 241 ERLGLTRQMVNPVRFYESVETMQKLGATRFLIEVGGRVLSGFIRKIDRNAEIANVNL 300

RESULT 11
 US-09-107-532-6973
 ; Sequence 6973, Application US/09107532
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A. Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; TITLE OF INVENTION: ENZYME PAECTUM FOR
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 7308
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM: CD/ROM ISO9660

COMPUTER: OPERATING SYSTEM:

SOFTWARE:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/ 085598

FILING DATE: May 14, 1998

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneka

REGISTRATION NUMBER: 40 489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6973:

SEQUENCE CHARACTERISTICS:

TYPE: amino acids

LENGTH: 328 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE: NAME/KEY: misc_feature

LOCATION: 1...328

NUMBER OF SEQUENCES: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM: CD/ROM ISO9660

COMPUTER: OPERATING SYSTEM:

SOFTWARE:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/ 085598

FILING DATE: May 14, 1998

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneka

REGISTRATION NUMBER: 40 489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6973:

SEQUENCE CHARACTERISTICS:

TYPE: amino acids

LENGTH: 328 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE: NAME/KEY: misc_feature

LOCATION: 1...328

RESULT 13
 PCT-US02-03987-10920
 / GENERAL INFORMATION: PCT/US02/03987
 / APPLICANT: Eliira Pharmaceuticals, Inc.
 / TITLE OF INVENTION: Identifying the Target of a Compound which Inhibits C
 / FILE REFERENCE: ELITRA.08VPC
 / CURRENT FILING DATE: 2002-02-02
 / PRIORITY APPLICATION NUMBER: PCT/US02/03987
 / PRIORITY FILING DATE: 2001-02-09
 / NUMBER OF SEQ ID NOS: 1410
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 10920
 / LENGTH: 313
 / TYPE: PRT
 / ORGANISM: Enterococcus faecalis
 / PCT-US02-03987-10920

Query Match 61.7%; Score 937; DB 1; Length 313;
 Best Local Similarity 61.9%; Pred. No. 3.5e-82; Mismatches 40; Indels 0; Gaps 0;
 Matches 187; Conservative 187; Query Match 61.7%; Score 937; DB 1; Length 313;
 Best Local Similarity 61.9%; Pred. No. 3.5e-82; Mismatches 40; Indels 0; Gaps 0;
 Matches 187; Conservative 187;

Qy 3 KTAIPLFGGAQVQYLGMRDFYDQYPIKETIDASQVQYDILTEDKLNQTRYQ 62
 Db 6 KTAIPLFGGAQVQYLGMRDFYDQYPIKETIDASQVQYDILTEDKLNQTRYQ 65

Qy 3 KTAIPLFGGAQVQYLGMRDFYDQYPIKETIDASQVQYDILTEDKLNQTRYQ 62
 Db 6 KTAIPLFGGAQVQYLGMRDFYDQYPIKETIDASQVQYDILTEDKLNQTRYQ 65

Qy 63 PAILATSVAYRLQKQYQDPMVAGLSIGEYSAVLSAGLDPEADAVLVAKGAYMEA 122
 Db 66 PAILTVSVAFYRLQKQGKTPDVMVAGLSIGEYSAVLSAGLDPEADAVLVAKGAYMEA 125

Qy 123 APADSGKMYAVLNTEPEVIEBEACOKASELGVVTPANNTPAQVVIAGEVAVDRAVELIQ 182
 Db 126 APQGTGRMVAVMNAEREVIEKAQOASAFGIVAPANNTPQOIVIGGEAVDQAYTLK 185

Qy 183 EAGAKRLIPLKVSGFPEHTLAQVSQKLAETLAQVSFSDFTCPPLVGNTEAAVQKEDIAQ 242
 Db 186 EAGVKMIPILNVSGFPEHTLAQPKSLQADLKLNFQTMQIPVSNITAEIMPQEAQA 245

Qy 243 LLTRQYKEPVYFESIGNQEAQISNFELIGPKVLSFGVKKIDQTAHLAHVEDQASIVVA 302
 Db 246 LLERQYMSAVRFEDSITEMKAMNGTMIEVGPGKLTIGFVKIDKTIEMHRVEDVATLIE 305

Qy 303 LL 304
 Db 306 TL 307

RESULT 15
 US-10-072-851-10920
 / Sequence 10320, Application US/10072851
 / GENERAL INFORMATION:
 / APPLICANT: Carr, Grant J.
 / APPLICANT: Xu, H. Howard
 / APPLICANT: Foulkes, Kari L.
 / APPLICANT: Zamudio, Carlos
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Ohisen, Kari L.
 / APPLICANT: Zyskind, Judith W.
 / APPLICANT: Wall, Daniel
 / APPLICANT: Travick, John D.
 / APPLICANT: Yamamoto, Robert T.
 / APPLICANT: Roemer, Terry
 / APPLICANT: Jiang, Bo
 / APPLICANT: Boone, Charles
 / APPLICANT: Bussey, Howard
 / TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
 / FILE REFERENCE: ELITRA.08A
 / CURRENT APPLICATION NUMBER: US/10/072,851
 / CURRENT FILING DATE: 2002-02-08
 / PRIORITY APPLICATION NUMBER: 60/267,636
 / PRIORITY FILING DATE: 2001-02-09
 / NUMBER OF SEQ ID NOS: 15811
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 10920
 / LENGTH: 313

RESULT 14
 US-09-815-242-10920
 / GENERAL INFORMATION: US/09815242
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Ohisen, Kari L.
 / APPLICANT: Zyskind, Judith W.
 / APPLICANT: Wall, Daniel
 / APPLICANT: Travick, John D.
 / APPLICANT: Carr, Grant J.
 / APPLICANT: Yamamoto, Robert T.
 / APPLICANT: Xu, H. Howard
 / TITLE OF INVENTION: Identification of Essential Genes in
 / FILE REFERENCE: ELITRA.011A
 / CURRENT APPLICATION NUMBER: US/09/815,242
 / CURRENT FILING DATE: 2001-03-21
 / PRIORITY APPLICATION NUMBER: 60/191,078
 / PRIORITY FILING DATE: 2000-03-21
 / PRIORITY APPLICATION NUMBER: 60/206,848
 / PRIORITY FILING DATE: 2000-05-23
 / PRIORITY APPLICATION NUMBER: 60/207,727
 / PRIORITY FILING DATE: 2000-05-26
 / PRIORITY APPLICATION NUMBER: 60/242,578

Query Match 61.7%; Score 937; DB 22; Length 313;
 Best Local Similarity 61.9%; Pred. No. 3.5e-82; Mismatches 40; Indels 0; Gaps 0;
 Matches 187; Conservative 187;

Qy 3 KTAIPLFGGAQVQYLGMRDFYDQYPIKETIDASQVQYDILTEDKLNQTRYQ 62
 Db 6 KTAIPLFGGAQVQYLGMRDFYDQYPIKETIDASQVQYDILTEDKLNQTRYQ 65

Qy 63 PAILATSVAYRLQKQYQDPMVAGLSIGEYSAVLSAGLDPEADAVLVAKGAYMEA 122
 Db 66 PAILTVSVAFYRLQKQGKTPDVMVAGLSIGEYSAVLSAGLDPEADAVLVAKGAYMEA 125

Qy 123 APADSGKMYAVLNTEPEVIEBEACOKASELGVVTPANNTPAQVVIAGEVAVDRAVELIQ 182
 Db 126 APQGTGRMVAVMNAEREVIEKAQOASAFGIVAPANNTPQOIVIGGEAVDQAYTLK 185

Qy 183 EAGAKRLIPLKVSGFPEHTLAQVSQKLAETLAQVSFSDFTCPPLVGNTEAAVQKEDIAQ 242
 Db 186 EAGVKMIPILNVSGFPEHTLAQPKSLQADLKLNFQTMQIPVSNITAEIMPQEAQA 245

Qy 243 LLTRQYKEPVYFESIGNQEAQISNFELIGPKVLSFGVKKIDQTAHLAHVEDQASIVVA 302
 Db 246 LLERQYMSAVRFEDSITEMKAMNGTMIEVGPGKLTIGFVKIDKTIEMHRVEDVATLIE 305

Qy 303 LL 304
 Db 306 TL 307

; TYPE: PRT
; ORGANISM: *Enterococcus faecalis*
US-10-072-81-10920

Query Match 61.7%; Score 937; DB 24; Length 313;

Best Local Similarity 61.9%; Pred. No. 3.5e-82;
Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

Qy 3 KTAAPLPGQQGAQYLGMGRDFDQYPVKEIDRASQVIGYDLYRLLDTBDDKLNQTRYTQ 62
Db 6 KTAAPLPGQQGAQYLGMGRDFDQYPVKEIDRASQVIGYDLYRLLDTBDDKLNQTRYTQ 62
Qy 63 PAILATSVAYIYRLQEKYQPPMVAGLISGEYALVAGALDFEAVALVARGAYMEA 122
Db 66 PAILTVSAYIYRLQEKYQPPMVAGLISGEYALVAGALDFEAVALVARGAYMEA 125
Qy 123 APADSGKRVAVINTPVVEITEACQKASELGVTPANYNTPAQIVAGEVAVDRAVELLQ 182
Db 126 APQGTGKRVAVAVNAEREVITEACQEAQFIVAPANYNTPOQIVIGGEVAVDQMTLIK 185
Qy 183 EAGAKRLIPLKVSQPFHTAILEPASOKLAETLAQVSFSDFCPLVGNTEAAMOKEDIAQ 242
Db 186 EAVVKRNPPLNSQPFHTAILEPASOKLAQDIAKUNFQNOIPVSNTAIMEPOAICDA 245
Qy 243 LLTRQVKEPVRFYESIGYMOEAGISNFIEIGPGKVLSGGFVYKIDQTAHLAHVEDOASIVA 302
Db 246 LLBKQVNSAVRFEDSTBTMKNNGTMIEVGGKTLTGFKDQTIEKHERVEDVATLIE 305
Qy 303 LL 304
Db 306 TL 307

Search completed: June 11, 2003, 20:10:43
Job time : 236 secs

GenCore version 5.1.6
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Copyright - protein search, using sw model

Run on: June 11, 2003, 20:03:47 ; search time 80 Seconds

Perfect score: 1518 Sequence: 1 MTKTAFLFLAGQAGAQYLGMR.....QTAHIAHVEDQASLVALKEK 306

Scoring table: BLOSUM62 Gapp 10.0 , Gapext 0.5

Searched: 1050967 seqs, 226864292 residues

Total number of hits satisfying chosen parameters: 1050967

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New: *
1: /cggn2_6/prodata/1/paa/1/PTC_NEW_COMBO.PEP: *
2: /cggn2_6/prodata/1/paa/1/ISO6_NEW_COMBO.PEP: *
3: /cggn2_6/prodata/1/paa/1/ISO7_NEW_COMBO.PEP: *
4: /cggn2_6/prodata/1/paa/1/ISO8_NEW_COMBO.PEP: *
5: /cggn2_6/prodata/1/paa/1/ISO9_NEW_COMBO.PEP: *
6: /cggn2_6/prodata/1/paa/1/ISO10_NEW_COMBO.PEP: *
7: /cggn2_6/prodata/1/paa/1/ISO60_NEW_COMBO.PEP: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1515	99.8	306	6	US-10-282-122A-73805	Sequence 73805, A	Sequence 73805
2	1048	73.0	306	6	US-10-282-122A-72188	Sequence 72188, A	Sequence 72188
3	1036	69.2	308	6	US-10-282-122A-1870	Sequence 1870, A	Sequence 1870
4	952	62.7	312	6	US-10-282-122A-74709	Sequence 74709, A	Sequence 74709
5	948	62.5	328	6	US-10-282-122A-57675	Sequence 57675, A	Sequence 57675
6	937	61.7	309	6	US-10-282-122A-56896	Sequence 56896, A	Sequence 56896
7	937	61.7	315	5	US-09-134-000C-4987	Sequence 4987, AP	Sequence 4987, AP
8	937	61.7	315	5	US-09-134-000C-4987	Sequence 4987, AP	Sequence 4987, AP
9	937	61.7	315	6	US-10-434-665-4987	Sequence 4987, AP	Sequence 4987, AP
10	713	47.0	308	6	US-10-282-122A-52133	Sequence 52133, A	Sequence 52133, A
11	669.5	44.1	317	6	US-10-369-493-3122	Sequence 3122, A	Sequence 3122, A
12	657.5	43.3	312	6	US-10-282-122A-77375	Sequence 77375, A	Sequence 77375, A
13	654	43.1	313	6	US-10-369-493-7325	Sequence 7325, A	Sequence 7325, A
14	649.5	42.8	310	6	US-10-282-122A-68370	Sequence 68370, A	Sequence 68370, A
15	647	42.6	318	6	US-10-282-122A-5205	Sequence 52405, A	Sequence 52405, A
16	646	42.6	306	6	US-10-369-493-19174	Sequence 19174, A	Sequence 19174, A
17	643.5	42.4	309	6	US-10-282-122A-56519	Sequence 56519, A	Sequence 56519, A
18	643.5	42.4	309	6	US-10-369-493-793	Sequence 793, AP	Sequence 793, AP
19	643.5	42.4	312	6	US-10-282-122A-58091	Sequence 58091, A	Sequence 58091, A
20	636	41.9	309	6	US-10-282-122A-78414	Sequence 78414, A	Sequence 78414, A
21	628.5	41.4	312	6	US-10-282-122A-67441	Sequence 67441, A	Sequence 67441, A
22	626	41.2	308	6	US-10-282-122A-59351	Sequence 59351, A	Sequence 59351, A
23	625	41.2	311	6	US-10-282-122A-75151	Sequence 75151, A	Sequence 75151, A
24	619	40.8	309	6	US-10-282-122A-57588	Sequence 57588, A	Sequence 57588, A
25	616.5	40.6	312	6	US-10-282-122A-66433	Sequence 66433, A	Sequence 66433, A

ALIGNMENTS

RESULT 1
US-10-282-122A-73805
; Sequence 73805, Application US/10282122A

; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cherry
; APPLICANT: Hasebeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forstner, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EIJTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/205,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/257,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PAIR.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 73805
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-10-282-122A-73805

Query Match 99.8%; Score 1515; DB 6; Length 306;
 Best Local Similarity 99.7%; Pred. No. 4.8e-124;
 Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTKTAFLFAGGQAQYLGMRDFYDQYIVKETIDRASQVLYGYDRLITDEEDLNQTRY 60
 Db 1 MTKTAFLFAGGQAQYLGMRDFYDQYIVKETIDRASQVLYGYDRLITDEEDLNQTRY 60

Qy 61 TQPAILATSVAYRLIQLQEGKQDPMVAGLSIGEYSAVSGALDFEDAVLVAKRGAYME 120
 Db 61 TQPAILATSVAYRLIQLQEGKQDPMVAGLSIGEYSAVSGALDFEDAVLVAKRGAYME 120

Qy 61 EAAPADSGKMYAVLNTPVIEEACOKASELGVVTPANTPAQIVIAGEVVAVDRAVEL 180
 Db 61 EAAPADSGKMYAVLNTPVIEEACOKASELGVVTPANTPAQIVIAGEVVAVDRAVEL 180

Qy 121 EAAPADSGKMYAVLNTPVIEEACOKASELGVVTPANTPAQIVIAGEVVAVDRAVEL 120
 Db 121 EAAPADSGKMYAVLNTPVIEEACOKASELGVVTPANTPAQIVIAGEVVAVDRAVEL 120

Qy 181 LOBAGAKRKLIPKVSFGPHTALLEPASQKLAEILAQVSDFTCPLVGNTEAAVQKEDI 240
 Db 181 LOBAGAKRKLIPKVSFGPHTALLEPASQKLAEILAQVSDFTCPLVGNTEAAVQKEDI 240

Qy 241 AQLITRQKEPVRFYSSIGMQEAGISNFIETIGPKVLSGFVRKIDQTHLAHVEDQASL 300
 Db 241 AQLITRQKEPVRFYSSIGMQEAGISNFIETIGPKVLSGFVRKIDQTHLAHVEDQASL 300

Qy 301 VALLEK 306
 Db 301 VALLEK 306

RESULT 2
 US-10-282-122A-72188
 Sequence 72188, Application US/10282122A
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cherry
 APPLICANT: Haseibek, Robert
 APPLICANT: Olsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 72288

Query Match 73.0%; Score 1108; DB 6; Length 306;
 Best Local Similarity 71.8%; Pred. No. 1.7e-88;
 Matches 37; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MTKTAFLFAGGQAQYLGMRDFYDQYIVKETIDRASQVLYGYDRLITDEEDLNQTRY 60
 Db 1 MTKTAFLFAGGQAQKGMASLYEIYDVKETFTHSITGVDYLIDDEEDLNQTRY 60

Qy 61 TQPAILATSVAYRLIQLQEGKQDPMVAGLSIGEYSAVSGALDFEDAVLVAKRGAYME 120
 Db 61 TQPAILATSVAYRLIQLQEGKQDPMVAGLSIGEYSAVSGALDFEDAVLVAKRGAYME 120

Qy 61 AQPAILTTSVAYRLIQLQEGKQDPMVAGLSIGEYSAVSGALDFEDAVLVAKRGFME 120

Qy 121 EAAPADSGKMYAVLNTPVIEEACOKASELGVVTPANTPAQIVIAGEVVAVDRAVEL 180
 Db 121 TAAPAGGKMYAVMTDPRLIEEICKASSKGIVSPANTNPTQVIGGVAAYDVAVEL 180

Qy 181 LOBAGAKRKLIPKVSFGPHTALLEPASQKLAEILAQVSDFTCPLVGNTEAAVQKEDI 240
 Db 181 LKGAGGSCRSLIKVSSPEFHALLKPSQKLAAQALENKTFDEMPLVGNTKAEIMKEQEI 240

Qy 241 AQLITRQKEPVRFYSSIGMQEAGISNFIETIGPKVLSGFVRKIDQTHLAHVEDQASL 300
 Db 241 KPLLARQKEPVRFYSSIGMQEAGISNFIETIGPKVLSGFVRKIDQTHLAHVEDQASL 300

Qy 301 VALLEK 306
 Db 301 VALLEK 306

RESULT 3
 US-10-369-493-18370
 Sequence 72189, Application US/10369493
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-1015205(B)
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO: 18370
 TYPE: PRT
 ORGANISM: Lactococcus lactis
 US-10-369-493-18370

Query Match 69.0%; Score 1048; DB 6; Length 308;
 Best Local Similarity 67.5%; Pred. No. 3e-83;
 Matches 208; Conservative 40; Mismatches 58; Indels 2; Gaps 1;

Qy 1 MTKTAFLFAGGQAQYLGMRDFYDQYIVKETIDRASQVLYGYDRLITDEEDLNQTRY 60
 Db 1 MTKTAFLFAGGQAQKGMARDLYQETVKATFBEASQALGYDRLNDDEEKLNEY 60

Qy 61 TQPAILATSVAYRLIQLQEGKQDPMVAGLSIGEYSAVSGALDFEDAVLVAKRGAYME 120
 Db 61 TQPAILATTSVAYRLIQLQEGKQDPMVAGLSIGEYSAVSGALDFEDAVLVAKRGQYNT 120

Qy 121 EAAPADSGKMYAVLNTPVIEEACOKASEL-GVVTPTANNTPAQIVIAGEVVAVDRAV 178
 Db 121 EAAPADSGKMYAVNTDPALIEEICQKAEEFKGSGIVSPANTPAQIVIAGEVVAVDIAV 180

RESULT 6
US-10-417-884-6973
; Sequence 6973. Application US/10417884
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FABICUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02454
COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/417,884
; FILING DATE: 17-APR-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinieillo, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTIC-012
; TELEPHONE: (781)893-8207
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6973:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...328
; SEQUENCE DESCRIPTION: SEQ ID NO: 6973 ;

RESULT 7
US-10-882-122A-56896
; Sequence 56896. Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRIA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614

US-10-417-884-6973
; Query Match 62.5%; Score 948; DB 64; Length 328;
; Best Local Similarity 61.6%; Pred. No. 1.8e-4;
; Matches 188; Conservative 63; Mismatches 4; Gaps 2;
;
Qy 63 PAILATSVAVTLLQEKYQPDIVASLIGYSALVAGLDPEAVAVAKRAYMEA 122
Db 61 PAILATSVAVTLLQEKYQPDIVASLIGYSALVAGLDPEAVAVAKRAYMEA 120
;
Qy 123 APADSGKQAVAVLNTPVVEEACQKASELGVTPANYNTPAQIVTAGEVAVDRAVELIQ 182
Db 121 APAGSGKQAVAVNAPIETEBSCEASKEYGIVSPANYNTPQIVIGGEKAVDEAVLIK 180
Qy 183 EAGAKRLIPLVKSPGPHTALEPAAKKLAKDLSQTQPSSESP1SNTTEIMKETAG 242
Db 181 EKGFRMPLVNSGPGPHTALEPAAKKLAKDLSQTQPSSESP1SNTTEIMKETAG 240
Qy 243 LLTROVKEPVRFYESIGPKVLSGPKVSKIDOTAHVHQDASL-- 300
Db 241 LLQQVNQKPVRFYESIKHLKIGIEQVIEVGPKVLSGPKVSKIDOTAHVHQDASL-- 300
;
Qy 301 -VALL 304
Db 301 TAIL 305
;
RESULT 6
US-10-417-884-6973
; Sequence 6973. Application US/10417884
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FABICUM FOR DIAGNOSTICS AND THERAPEUTICS

Query Match 62.5%; Score 948; DB 64; Length 328;
Best Local Similarity 61.6%; Pred. No. 1.8e-4;
Matches 188; Conservative 63; Mismatches 4; Gaps 2;
;
Qy 3 KTAFLFGQGQAOYLGMDPFDYQPVKETIDRASSVIGDYLRLDTEEDKLNQTRYQ 62
Db 25 KTAFLFGQGQAOYLGMDPFDYQPVKETIDRASSVIGDYLRLDTEEDKLNQTRYQ 63
;
Qy 63 PAILATSVAVTLLQEKYQPDIVASLIGYSALVAGLDPEAVAVAKRAYMEA 122
Db 94 PAILATSVAVTLLQEKYQPDIVASLIGYSALVAGLDPEAVAVAKRAYMEA 143
;
Qy 123 APADSGKQAVAVLNTPVVEEACQKASELGVTPANYNTPAQIVTAGEVAVDRAVELIQ 182
Db 144 PAGSGKQAVAVNAPIETEBSCEASKEYGIVSPANYNTPQIVIGGEKAVDEAVLIK 203
;
Qy 183 EAGAKRLIPLVKSPGPHTALEPAAKKLAKDLSQTQPSSESP1SNTTEIMKETAG 242
Db 204 EKGFRMPLVNSGPGPHTALEPAAKKLAKDLSQTQPSSESP1SNTTEIMKETAG 263
;
Qy 243 LLTROVKEPVRFYESIGPKVLSGPKVSKIDOTAHVHQDASL-- 300
Db 264 LLQQVNQKPVRFYESIKHLKIGIEQVIEVGPKVLSGPKVSKIDOTAHVHQDASL-- 300
;
Qy 301 -VALL 304
Db 324 TAIL 328
;

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 56896

LENGTH: 309

TYPE: PRF

ORGANISM: Enterococcus faecalis

US-10-284-1224-56896

Query Match 61.7%; Score 937; DB 6; Length 309;

Best Local Similarity 61.9%; Pred. No. 1.5e-73;

Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

Qy 3 KTAFLPAGGAQIYLGMRFYDQPIVETIDPASQVIGDYLRLIDTEDKLINQTRYTQ 62

Db 2 KTAIIFSGGAQIYQGMGEIYHQAIVRTEDASHIILGYEVAELCTTENERLINEYETQ 61

Qy 63 PAILATSVATYRLLQEKGKQPDNAGLSGEYSALVAGALDPEAVLVAKGAYMEA 122

Db 62 PAILTVSAYRLLQQKGITPDVYAGLSGEYSALVAGALRSEAVLVAQERGQNTTEA 121

Qy 123 APADSGKMYAVLNTPVEVIEACOASEIGVUTPANTTPAQIVIAGEVVAVDRAVELLQ 182

Db 122 APQGTGKMYAVMNAREVIEKACOASEAAGIVAPANTTPQQIVIGEVVAVDQMTLLK 181

Qy 183 EAGAKRLIPIKVVSQSPFHTLLEPASQVFLAETLQAVSFSDFTCPLVGTGTEAAMQKEDIAQ 242

Db 182 EAGVKRMIPAVNSGPFHTLQPLASKLQADLAKINFQTMQIPFVNSNTAEIMQEAQIA 241

Qy 243 LLTRQVKEPYRPFYESIGNVQEAQISNF1EIGPKEVLSGFVKKIDOTAHVAYEDOASLVA 302

Db 242 LLERQYMSAVRFEDSIETNMKAMNYGTMIEVGPKTTLGFKVVKIDKTIEMHRVEDVATLIE 301

Qy 303 LL 304

Db 302 TL 303

RESULT 8

US-09-134-000C-4987

Sequence 4987, Application US/09134000C

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134, 000C

CURRENT FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 4987

LENGTH: 315

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-4987

Query Match 61.7%; Score 937; DB 5; Length 315;

Best Local Similarity 61.9%; Pred. No. 1.5e-73;

Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

Qy 3 KTAFLIAGQGAQIYLGMRFYDQPIVETIDPASQVIGDYLRLIDTEDKLINQTRYTQ 62

Db 8 KTAIIFSGGAQIYQGMGEIYHQAIVRTEDASHIILGYEVAELCTTENERLINEYETQ 67

Qy 63 PAILATSVATYRLLQEKGKQPDNAGLSGEYSALVAGALDPEAVLVAKGAYMEA 122

Db 68 PAILTVSAYRLLQGKQPDNAGLSGEYSALVAGALRSEAVLVAQERGQNTTEA 127

Qy 123 APADSGKMYAVLNTPVEVIEACOASEIGVUTPANTTPAQIVIAGEVVAVDRAVELLQ 182

Db 122 APQGTGKMYAVMNAREVIEKACOASEAAGIVAPANTTPQQIVIGEVVAVDQMTLLK 187

Qy 183 EAGAKRLIPIKVVSQSPFHTLLEPASQVFLAETLQAVSFSDFTCPLVGTGTEAAMQKEDIAQ 242

Db 188 EAGVKRMIPAVNSGPFHTLQPLASKLQADLAKINFQTMQIPFVNSNTAEIMQEAQIA 247

Qy 243 LLTRQVKEPYRPFYESIGNVQEAQISNF1EIGPKEVLSGFVKKIDOTAHVAYEDOASLVA 302

Db 248 LLERQYMSAVRFEDSIETNMKAMNYGTMIEVGPKTTLGFKVVKIDKTIEMHRVEDVATLIE 307

Qy 303 LL 304

Db 302 TL 303

RESULT 10

US-10-434-665-4987

Sequence 4987, Application US/10434665

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FILE REFERENCE: PATH3-09

CURRENT APPLICATION NUMBER: US/10/434, 665

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 4987

LENGTH: 315

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-4987

Query Match 61.7%; Score 937; DB 5; Length 315;

Best Local Similarity 61.9%; Pred. No. 1.5e-73;

Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

Qy 3 KTAFLPAGGAQIYLGMRFYDQPIVETIDPASQVIGDYLRLIDTEDKLINQTRYTQ 62

Db 8 KTAIIFSGGAQIYQGMGEIYHQAIVRTEDASHIILGYEVAELCTTENERLINEYETQ 67

Qy 63 PAILATSVATYRLLQEKGKQPDNAGLSGEYSALVAGALDPEAVLVAKGAYMEA 122

Db 68 PAILTVSAYRLLQQKGITPDVYAGLSGEYSALVAGALRSEAVLVAQERGQNTTEA 127

Qy 123 APADSGKMYAVLNTPVEVIEACOASEIGVUTPANTTPAQIVIAGEVVAVDRAVELLQ 182

Db 128 APQGTGKMYAVMNAREVIEKACOASEAAGIVAPANTTPQQIVIGEVVAVDQMTLLK 187

Qy 183 EAGAKRLIPIKVVSQSPFHTLLEPASQVFLAETLQAVSFSDFTCPLVGTGTEAAMQKEDIAQ 242

Qy 303 LL 304

Db 302 TL 303

RESULT 11

US-10-434-665-4987

Sequence 4987, Application US/10434665

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FILE REFERENCE: PATH3-09

CURRENT APPLICATION NUMBER: US/10/434, 665

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 4987

LENGTH: 315

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-4987

Query Match 61.7%; Score 937; DB 5; Length 315;

Best Local Similarity 61.9%; Pred. No. 1.5e-73;

Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

Qy 3 KTAFLPAGGAQIYLGMRFYDQPIVETIDPASQVIGDYLRLIDTEDKLINQTRYTQ 62

Db 8 KTAIIFSGGAQIYQGMGEIYHQAIVRTEDASHIILGYEVAELCTTENERLINEYETQ 67

Qy 63 PAILATSVATYRLLQEKGKQPDNAGLSGEYSALVAGALDPEAVLVAKGAYMEA 122

Db 68 PAILTVSAYRLLQQKGITPDVYAGLSGEYSALVAGALRSEAVLVAQERGQNTTEA 127

Qy 123 APADSGKMYAVLNTPVEVIEACOASEIGVUTPANTTPAQIVIAGEVVAVDRAVELLQ 182

Db 128 APQGTGKMYAVMNAREVIEKACOASEAAGIVAPANTTPQQIVIGEVVAVDQMTLLK 187

Qy 183 EAGAKRLIPIKVVSQSPFHTLLEPASQVFLAETLQAVSFSDFTCPLVGTGTEAAMQKEDIAQ 242

Qy 303 LL 304

Db 302 TL 303

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; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4987
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-10-134-655-4987

Query Match 61.7% Score 937; DB 6; Length 315;
Best Local Similarity 61.9%; Pred. No. 1.5e-73; Mismatches 40; Indels 0; Gaps 0;
Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;
Organism: Clostridium acetobutylicum
US-10-262-122A-5213

; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4987
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
; US-10-262-122A-5213

Query Match 47.0% Score 713.5; DB 6; Length 308;
Best Local Similarity 40.5%; Pred. No. 4.9e-54; Mismatches 56; Indels 3; Gaps 3;
Matches 147; Conservative 56; Mismatches 97; Indels 3; Gaps 3;
Organism: Clostridium acetobutylicum
US-10-262-122A-5213

; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5213
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
; US-10-262-122A-5213

Query Match 40.5% Score 713.5; DB 6; Length 308;
Best Local Similarity 40.5%; Pred. No. 4.9e-54; Mismatches 56; Indels 3; Gaps 3;
Matches 147; Conservative 56; Mismatches 97; Indels 3; Gaps 3;
Organism: Clostridium acetobutylicum
US-10-262-122A-5213

; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 7814
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5213

Query Match 1 MTKTAFLAGQGAQYLGMRDFDQYPIVKETIDRASQVLYGDRYL-IDTEEDKLKNOTR 59
; Best Local Similarity 40.5%; Pred. No. 4.9e-54; Mismatches 56; Indels 3; Gaps 3;
; Matches 147; Conservative 56; Mismatches 97; Indels 3; Gaps 3;
; Organism: Clostridium acetobutylicum
; US-10-262-122A-5213

; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 7814
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5213

Query Match 1 MGKIAFVPSQGQSYQVMGRDLYQSAKETTDKADEVLGKISELPEGDEELNLTE 60
; Best Local Similarity 40.5%; Pred. No. 4.9e-54; Mismatches 56; Indels 3; Gaps 3;
; Matches 147; Conservative 56; Mismatches 97; Indels 3; Gaps 3;
; Organism: Clostridium acetobutylicum
; US-10-262-122A-5213

Db 1 NTQPAVLTSIAALRALEBKG1KPDVAGLSGEYSAHVCSSSFSPDAVLVKKERY 120
Db 1 MEEAPADSGRMVAVLNTPVEVTEACQAKASELGVVTANNTPAQVHAGEVVAVDBAV 178
Db 1 YTOPPAILATSVATRLL-QEKGYOPDMYAGLSEGEYSAVASSALDFDAAVALVAKRGAY 118
Db 1 NTQPAVLTSIAALRALEBKG1KPDVAGLSGEYSAHVCSSSFSPDAVLVKKERY 120

Query Match 60 YTOPPAILATSVATRLL-QEKGYOPDMYAGLSEGEYSAVASSALDFDAAVALVAKRGAY 118
; Best Local Similarity 40.5%; Pred. No. 4.9e-54; Mismatches 56; Indels 3; Gaps 3;
; Matches 147; Conservative 56; Mismatches 97; Indels 3; Gaps 3;
; Organism: Clostridium acetobutylicum
; US-10-262-122A-5213

Db 119 MEEAPADSGRMVAVLNTPVEVTEACQAKASELGVVTANNTPAQVHAGEVVAVDBAV 178
Db 121 MQBAPKGIGTMAAIGLEGDVVRGICAQOSKEGIVEVANYNCPGQVHAGEVVAVDBAV 180
Db 122 EDIAOLLTROKYPEPYRFYSSIGNQEAQISNFIB1GPKVLSFPRVCTIDQTAHLAHYEDQASLVA 302
Db 123 EAGAKRLIPLKVSGPHTALLEPASQKLAETLQVSFDDFTPLVGNTEAAWQKEDIAQ 242
Db 124 ELLQGAKRLIPLKVSGPHTALLEPASQKLAETLQVSFDDFTPLVGNTEAAWQKEDIAQ 242
Db 125 DQIKGILKQKYMSSYRVEDTIRMMDDGYDTFIELGPKTLSSPIKKINRKMTIENIBKA 300
Db 126 EDIAOLLTROKYPEPYRFYSSIGNQEAQISNFIB1GPKVLSFPRVCTIDQTAHLAHYEDQ 297
Db 127 TKLKGSGARTVMSVSGPHTMSLKAEEKLEELRNINIEDMKVPUVNTVGDYVEDK 240
Db 128 DQIKGILKQKYMSSYRVEDTIRMMDDGYDTFIELGPKTLSSPIKKINRKMTIENIBKA 300
Db 129 ASL 300
Db 130 EDL 303

; PRIOR APPLICATION NUMBER: 60/369,493-23122
; CURRENT APPLICATION NUMBER: US-10-369,493-23122
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 4734
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Bacillus subtilis
; US-10-369-493-23122

Query Match 44.1% Score 669.5; DB 6; Length 317;
Best Local Similarity 47.2%; Pred. No. 3.6e-50; Mismatches 47; Indels 3; Gaps 3;
Matches 143; Conservative 47; Mismatches 110; Indels 3; Gaps 3;
Organism: Bacillus subtilis
US-10-369-493-23122

; PRIOR APPLICATION NUMBER: 60/360,039
; CURRENT APPLICATION NUMBER: US-10-369,493
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 4734
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Bacillus subtilis
; US-10-369-493-23122

Query Match 44.1% Score 669.5; DB 6; Length 317;
Best Local Similarity 47.2%; Pred. No. 3.6e-50; Mismatches 47; Indels 3; Gaps 3;
Matches 143; Conservative 47; Mismatches 110; Indels 3; Gaps 3;
Organism: Bacillus subtilis
US-10-369-493-23122

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1	MSKTAFLFFGQGSQFIGMGKELYEQVPAKRLFDEADETLERKLSSLIFEDDAEELITY	60	Best Local Similarity 47.4%; Pred. No. 3.9e-49; Matches 146; Conservative 58; Mismatches 97; Indels 7; Gaps 4;
60	YTQPAILATSVAYRLLQEKGYQPDMDYASALGEYSALVAGSALDFEDAVALVAKRGAYM	119	Qy
61	NAQPAILATSVIALEKFKESGTTDFTAGHSLEYSALVAGALSFKDAYTVRKGEM	120	Qy
120	EEAPADGGKMYAVINTPVEVIEBACQKASELG-VITPANNTPAQIVIAEVVAVDRAY	178	Db
121	NEAVPAGEMAMAAILGMDAELKQVTKVTKTETGNYLQGANUNCPGQIVISSTAKGYELAS	180	Db
179	ELIEQAGAKRLPLKVSPPHTALLEPASQKAETLAQVSFSDFTPLVGNTTEAAW-QK	237	Qy
181	ELAKENGAKRAILEVSCPFHSELMKPAAEKUKEVLDACIDKADPVIISVSDYMTK	240	Db
238	EDIAQLITRQVKEPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ	297	Qy
241	ADIKEKLQJELQYSPVRFEESSINKLIAEGVTTIEBIEGPKVLSGLVKKVNRLPLKTIAVSDP	300	Db
298	ASL 300	306	Qy
301	ETI 303	304	Db
RESULT 13			
Sequence 77375, Application US/10282122A			
GENERAL INFORMATION:			
APPLICANT:	Wang, Liangsu	305	Qy
APPLICANT:	Zamudio, Carlos	306	Db
APPLICANT:	Malone, Cheryl	307	Qy
APPLICANT:	Haselbeck, Robert	308	Db
APPLICANT:	Ohlsen, Kari	309	Qy
APPLICANT:	Zyskind, Judith	310	Db
APPLICANT:	Wall, Daniel	311	Qy
APPLICANT:	Trawick, John	312	Db
APPLICANT:	Carr, Grant	313	Qy
APPLICANT:	Yamamoto, Robert	314	Db
APPLICANT:	Forstyt, R.	315	Qy
APPLICANT:	Xu, H.	316	Db
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms			
FILE REFERENCE: EULTRA.034A			
CURRENT APPLICATION NUMBER: US/10/282,122A			
CURRENT FILING DATE: 2003-07-20			
PRIOR APPLICATION NUMBER: 60/191,078			
PRIOR FILING DATE: 2000-03-21			
PRIOR APPLICATION NUMBER: 60/206,848			
PRIOR FILING DATE: 2000-05-23			
PRIOR APPLICATION NUMBER: 60/207,727			
PRIOR FILING DATE: 2000-05-26			
PRIOR APPLICATION NUMBER: 60/230,335			
PRIOR FILING DATE: 2000-09-06			
PRIOR APPLICATION NUMBER: 60/230,347			
PRIOR FILING DATE: 2000-09-09			
PRIOR APPLICATION NUMBER: 60/242,578			
PRIOR FILING DATE: 2000-10-23			
PRIOR APPLICATION NUMBER: 60/253,625			
PRIOR FILING DATE: 2000-11-27			
PRIOR APPLICATION NUMBER: 60/257,931			
PRIOR APPLICATION NUMBER: 60/267,636			
PRIOR FILING DATE: 2001-02-09			
PRIOR APPLICATION NUMBER: 60/269,308			
PRIOR FILING DATE: 2001-02-16			
Remaining Prior Application data removed - See File Wrapper or PALM.			
NUMBER OF SEQ ID NOS: 78614			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO: 77375			
LENGTH: 312			
TYPE: PRT			
ORGANISM: Vibrio cholerae			
US-10-282-122A-77375			
RESULT 14			
US-10-369-493-17325			
; Sequence 17325, Application US/10369493			
; GENERAL INFORMATION:			
APPLICANT:	Cao, Yongwei	174	Qy
APPLICANT:	Hinkle, Gregory J.	175	Db
APPLICANT:	Slater, Steven C.	176	Qy
APPLICANT:	Goldman, Barry S.	177	Db
APPLICANT:	Chen, Yanfeng	178	Qy
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION			
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES			
; CURRENT APPLICATION NUMBER: US/10/369,493			
; CURRENT FILING DATE: 2003-02-28			
; PRIORITY APPLICATION NUMBER: 38-10 (52052) B			
; FILE REFERENCE: 38-10 (52052) B			
; CURRENT APPLICATION NUMBER: US/10/360,039			
; CURRENT FILING DATE: 2002-02-21			
; NUMBER OF SEQ ID NOS: 47374			
; SEQ ID NO: 17325			
; LENGTH: 313			
; TYPE: PRT			
; ORGANISM: Bacillus halodurans			
; US-10-369-493-17325			
Query Match 43.1%; Score 654; DB 6; Length 313;			
Best Local Similarity 45.6%; Pred. No. Be-49; Matches 106; Indels 4; Gaps 4;			
Matches 141; Conservative 58; Mismatches 106; Indels 6; Gaps 4;			
RESULT 15			
US-10-369-493-17325			
; Sequence 17325, Application US/10369493			
; GENERAL INFORMATION:			
APPLICANT:	Cao, Yongwei	179	Qy
APPLICANT:	Hinkle, Gregory J.	180	Db
APPLICANT:	Slater, Steven C.	181	Qy
APPLICANT:	Goldman, Barry S.	182	Db
APPLICANT:	Chen, Yanfeng	183	Qy
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION			
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES			
; CURRENT APPLICATION NUMBER: US/10/369,493			
; CURRENT FILING DATE: 2003-02-28			
; PRIORITY APPLICATION NUMBER: 38-10 (52052) B			
; FILE REFERENCE: 38-10 (52052) B			
; CURRENT APPLICATION NUMBER: US/10/360,039			
; CURRENT FILING DATE: 2002-02-21			
; NUMBER OF SEQ ID NOS: 47374			
; SEQ ID NO: 17325			
; LENGTH: 313			
; TYPE: PRT			
; ORGANISM: Bacillus halodurans			
; US-10-369-493-17325			
Query Match 43.1%; Score 654; DB 6; Length 313;			
Best Local Similarity 45.6%; Pred. No. Be-49; Matches 106; Indels 4; Gaps 4;			
Matches 141; Conservative 58; Mismatches 106; Indels 6; Gaps 4;			
RESULT 16			
1 MTKTAFLFFGQGAQYLGMGRDFDQYPTKETIDRASQVLYGLYDYLRL-DTEBDKLNOT 59			
6 MSKTAFLFFGQGAQYLGMGRDFDQYPTKETIDRASQVLYGLYDYLRL-DTEBDKLNOT 65			
60 YTQPAILATSVAYRLLQEKGY-QPDMDVAGLSGEYSALVAGSALDFEDAVALVAKRGAYM 118			
66 RTQPAILATSVAYRLLQEKGY-QPDMDVAGLSGEYSALVAGSALDFEDAVALVAKRGOL 125			
119 MEEAAPADSGKMYAVINTVEVIEBACQKASELG-VITPANNTPAQIVIATGEVYAVDRAY 178			
126 MQQAVPAGTGMAYVAVLNTVEVIEBACQKASELG-VITPANNTPAQIVIATGEVYAVDRAY 185			
128 EDIAQLITRQVKEPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ			
179 ELLQAGAKRLPLKVSPPHTALLEPASQKAETLAQVSFSDFTPLVGNTTEAAW-QK 178			
180 EEAKEGAKRVLPLQVSPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ 179			
182 EEAKEGAKRVLPLQVSPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ 179			
186 VLGKEAGAKRVLPLQVSPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ 179			
188 EEAKEGAKRVLPLQVSPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ 179			
190 EEAKEGAKRVLPLQVSPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ 179			
192 EEAKEGAKRVLPLQVSPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ 179			
194 EEAKEGAKRVLPLQVSPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ 179			
196 EEAKEGAKRVLPLQVSPVRFVYESIGMQBAGISNFNIEBIEGKVLGFGVAKIDQTAHLAHEVDQ 179			
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 Qy 298 ASLVALL 306 Qy 238 EDIAQLTROCKEPRVFTESIGNMQEAGISNFIEGSPKULSFVKKIDQTAHLAHEVDQ 297
 Db 300 ASLFAAMXK 308 Db 241 NAIRDALVQOLYNFRWIEVFLAGKGTQLLBIGPSKVLGLTRRISKEMNAAVNDI 300
 Qy 298 ASLVALL 304
 Db 301 ASLDAL 307

RESULT 15
 US-10-282-122A-68370
 i Sequence 65370, Application US/10282122A
 i GENERAL INFORMATION:
 i APPLICANT: Wang, Liangshu
 i APPLICANT: Zamudio, Carlos
 i APPLICANT: Malone, Cherry
 i APPLICANT: Haselbeck, Robert
 i APPLICANT: Ohlsen, Kari
 i APPLICANT: Zyskind, Judith
 i APPLICANT: Wall, Daniel
 i APPLICANT: Trawick, John
 i APPLICANT: Carr, Grant
 i APPLICANT: Yamamoto, Robert
 i APPLICANT: Forsyth, Robert
 i APPLICANT: Xu, H.
 i TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 i FILE REFERENCE: ELTRA 034A
 i CURRENT APPLICATION NUMBER: US/10/282,122A
 i CURRENT FILING DATE: 2003-05-20
 i PRIOR APPLICATION NUMBER: 60/191,078
 i PRIOR FILING DATE: 2000-03-21
 i PRIOR APPLICATION NUMBER: 60/206,848
 i PRIOR FILING DATE: 2000-05-23
 i PRIOR APPLICATION NUMBER: 60/207,727
 i PRIOR FILING DATE: 2000-05-26
 i PRIOR APPLICATION NUMBER: 60/230,335
 i PRIOR FILING DATE: 2000-09-06
 i PRIOR APPLICATION NUMBER: 60/230,347
 i PRIOR FILING DATE: 2000-09-09
 i PRIOR APPLICATION NUMBER: 60/242,578
 i PRIOR FILING DATE: 2000-10-23
 i PRIOR APPLICATION NUMBER: 60/253,625
 i PRIOR FILING DATE: 2000-11-27
 i PRIOR APPLICATION NUMBER: 60/257,931
 i PRIOR FILING DATE: 2000-12-22
 i PRIOR APPLICATION NUMBER: 60/267,636
 i PRIOR FILING DATE: 2001-02-09
 i PRIOR APPLICATION NUMBER: 60/269,308
 i PRIOR FILING DATE: 2001-02-16
 i Remaining Prior Application data removed - See File Wrapper or PALM.
 i NUMBER OF SEQ ID NCS: 78614
 i SOFTWARE: Patentin version 3.1
 i SEQ ID NO: 68370
 i LENGTH: 310
 i TYPE: PRT
 i ORGANISM: Proteus mirabilis
 US-10-282-122A-68370

Query Match 42.8%; Score 649.5; DB 6; Length 310;
 Best Local Similarity 47.2%; Pred. No. 1.9e-48; Mismatches 108; Index 3; Gaps 3;
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 Qy 60 YTOPAILATSVAIYRJICK-GYQPDWYAGLSLGEYSALVAGALDFBDAVALVAKRGAV 118
 Db 61 KTOPAILATSVAIWRWQEKQGMPQMAHGEYSALVAGVIFDAAIKLVBLRGQL 120
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 Db 121 MQAVPACTGMYAATGNDATAKACEDAAQGVSPVFNPGQYVIGKNERVERAG 180
 Qy 179 ELLQEAGAKRLLPLKVSQPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEA-AMVQK 237

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 11, 2003, 20:17:43 ; Search time 2196 Seconds
 (without alignments)

Perfect score: 1518

Sequence: 1 MTKTAFLFAGQGAQYLGMR.....QTAHLAHVEDQASIVALEK 306

Scoring table: BLCSUM62

Xgapop 10.0 ; Xgapext 0.5
 Ygapop 10.0 ; Ygapext 0.5
 Fgapop 6.0 ; Fgapext 7.0
 Delext 6.0 ; Delext 7.0

Searched: 24791104 seqs, 1257124825 residues

Total number of hits satisfying chosen parameters: 495822208

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution and is derived by analysis of the result being printed.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
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2	1518	100 0	921	22	US-09-308-397-1 Sequence 1251, Appl
3	1518	100 0	921	29	US-09-308-397-1 Sequence 30, Appl
4	1518	100 0	921	61	US-09-308-397-1 Sequence 30, Appl
5	1518	100 0	924	15	US-09-107-433-794 Sequence 794, Appl
c	6	1518	100 0	19702	41 US-10-158-844-7 Sequence 7, Appl

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7	1518	100.0	19706	46 US-60-029-960-61			
8	1515	99.8	945	29 US-60-052-969-56			
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10	1514	99.7	921	1 PCU-US02-033897-9482			
11	1514	99.7	921	31 US-09-015-242-9482			
12	1514	99.7	921	39 US-10-012-851-1512			
13	1514	99.7	9753	50 US-60-068-175-555			
14	1488	98.0	5963	50 US-60-061-998-494			
15	1048-	69.0	927	80 US-60-160-0-39-4205			
16	952	62.7	2969	49 US-60-050-0-44-527			
17	952	62.7	2969	50 US-60-168-1-86-533			
18	948	62.5	987	15 US-09-1-86-532-3319			
19	948	62.5	987	15 US-09-10-532-1319			
20	937	61.7	942	31 PCU-US03-03987-6823			
21	937	61.7	942	31 US-09-815-242-6823			
22	937	61.7	942	39 US-10-072-851-6823			
23	937	61.7	948	39 US-09-13-4-000-1562			
24	920	60.6	3656	14 US-09-070-027-577			
25	920	60.6	3656	14 US-09-070-927A-577			
26	863	56.9	547	17 US-09-10-377-5			
27	858	56.5	1196	1 PCU-US97-07980-8			
28	858	56.5	1199	12 US-08-832-030-78			
29	858	56.5	1209	16 US-09-297-151-81			
30	858	56.5	1209	16 US-09-297-411-81			
31	830	54.7	3627	48 US-60-045-449-929			
32	830	54.7	3627	48 US-60-046-553-916			
33	830	54.7	3627	50 US-60-168-217-803			
34	6715	44.2	6336	12 US-08-832-030-157			
35	669.5	44.1	954	80 US-60-160-0-39-44809			
36	654	43.1	942	80 US-60-16-0-39-41012			
37	648.5	42.7	1002	21 US-09-143-661-3811			
38	646	42.6	918	21 US-60-160-0-39-42861			
39	646	42.6	942	34 US-09-902-540-7557			
40	646	42.6	5467	34 US-09-902-540-703			
41	643.5	42.4	930	31 PCU-US02-03987-6028			
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45	636	41.9	930	39 US-10-16-0-39-42440			
46	636	41.9	930	39 PCU-US02-03987-6028			
47	6878	40.9	930	39 US-10-16-0-39-42440			
48	6878	40.9	930	39 PCU-US02-03987-6028			

ALIGNMENTS

RESULT 1
US-09-308-397-1
Sequence 1, Application US/09308397
GENERAL INFORMATION
APPLICANT: Gentry, Daniel R.
APPLICANT: Lonsdale, John T.
APPLICANT: Payne, David J.
APPLICANT: Pearson, Stewart C.
APPLICANT: Van Aller, Glenn
TITLE OF INVENTION: Novel FabD
FILE REFERENCE: PS0593
CURRENT APPLICATION NUMBER: US/09/308 397
CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: US 60/031,160
EARLIER FILING DATE: 1996-11-18
EARLIER APPLICATION NUMBER: PCT/US97/20992
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 921
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-308-397-1

Alignment Scores:
Seq. No.: 1 Length: 921
Score: 1.58e-141 Matches: 306
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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201 AlaIleLeuGluProAlaSerGlnLysLeuAlaGluIleLeuAlaGlnValSerPheser 220
601 GCTCTCTTGACCTGCTAGCCGAAACTAGTGAACTCTAGCTAGTTCA 660
221 AspPheThrCysProLeuValGlyAspThrGluAlaAlaAlaValMetGlnLysGluAspIle 240
661 GATTTACTTGCCCCCTAGTCGCAATAAGAGCTGATGAAAGGACATT 720
241 AlaGlnIleLeuThrArgGlnValIysGluProValArgPheTerGlyVal 260
721 GCTAGCTCTGAGCAGCTGATGAAAGTATGGGTC 780
261 MetGlnGluAlaAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
781 ATGCAAGAGCAGGCAATAGGCAACTTATCGATGGACATTATCGATGGCTGTGAGGT 840
281 ProValLysLysIleAspGlnIleAspGlnAlaAspLeu 300
841 TTGTGTAAAAATATTGATCAAATGCTCACTTAGCTCATGTAAGATAAGCGAGTTA 900
301 ValAlaLeuGluLys 306
901 GTAGCACTTTAGAAAA 918

RESULT 2
US-09-563-110-1251
Sequence 1251, Application US/09583110
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus FILE REFERENCE: PATE00-07A
 CURRENT APPLICATION NUMBER: US/09/583,110
 CURRENT FILING DATE: 2000-05-26
 PRIORITY NUMBER: US 09/107,433
 PRIORITY FILING DATE: 1998-06-30
 PRIORITY NUMBER: US 60/085,131
 PRIORITY FILING DATE: 1998-05-12
 PRIORITY APPLICATION NUMBER: US 60/051,553
 PRIORITY FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 5322
 SEQ ID NO: 1251
 LENGTH: 921
 TYPE: DNA
 ORGANISM: Streptococcus pneumoniae
 US-09-583-110-1251

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Qy	21	AspPheTyrAspGlnTyrProIleValYsGluThrIleAspPheAlaSerGlnValLeu	40	0	0
Db	61	GATTATGATGATGATGCCATGTTAAACAAACATTGATGACGGTCAGGCTC	120	0	0
Qy	41	GLYTyrAspLeuArgTyrLeuIleAspThrGluGluAspIleValAsnGlnThrArgTyr	60	0	0
Db	121	GTTATGATTGCGTTATCTATCGATACCGAAAGGACAACTCATGACCCCTAT	180	0	0
Qy	61	ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuGlnGluLysGly	80	0	0
Db	181	ACGCAACCGCCATTAGCCTACTGGTGTCTATACCGTTATGCAAGAAAGGGC	240	0	0
Qy	81	TyrGinProAspMetValAlaGlyLeuSerIeuGlyGluTyrSerIleLeuAlaSer	100	0	0
Db	241	TATCGCCGTATGATGTCGCTGTTGCTTGGAAATCTCGCCCTGGGAAAGC	300	0	0
Qy	101	GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrNetGlu	120	0	0
Db	301	GGCGCTTGATTTCAAGTCGGGTTGCTGAGCTAGCGTGAGCTATAGGAA	360	0	0
Qy	121	GluAlaAlaAlaPheAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGlu	140	0	0
Db	361	GAAGCGGCCTCTGTGACTCTGGCAGATGCTAGCTGAGTCTCAATGCGCAGTAGGGTC	420	0	0
Qy	141	IleGluGluAlaCysGlnIysAlaSerGlnGluIeuGlyValAlaIleAsnTyrAsn	160	0	0
Db	421	ATTTGAAAGGCCTGTCGAAAGCTCTGAACTTGGTGTACTCCAGCCAACTATAAC	480	0	0
Qy	161	ThrProAlaGinIleValLeuAlaGlyGluValValAlaLysArgLeuIleProIleLysValGlu	180	0	0
Db	481	ACACCTGGCAZAAATGCTATGCTGAGAAGTGTGAGCTGAGTGTGACTT	540	0	0
Qy	181	LeuGinGluAlaGlyAlaIleAspGluIleProIleLysValGlyProPheHisThr	200	0	0
Db	541	TTGGCAAGAGGCTCCAAAGCTCTAAGGCTGAGTCGTCAGTCCTTCAAC	600	0	0
Qy	201	AlaLeuLeuGluProAlaSerGlnIysLeuAlaGluIleLeuAlaGlnValSerPheSer	220	0	0
Db	601	GCTTCCTGGCAACCTGGCAACACTGGTAACTGAAACTCTGGTAACTGGAA	660	0	0

QY 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaAlaValMetGlnLysGluAspIle 240
 Db 661 GATTCTACTGCCCCTAGTCGGCATACGAAAGTCATGATCANAAGGGCATT 720
 QY 241 AlaGlnLeuLeuThrArgGlnValIysGluProValArgPheTerGluSerIleGlyVal 260
 Db 721 GCTCGCTCTGACCGTCAGGTCAGAACCCGTCGTTCTAGAAAGTATGGTC 780
 QY 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
 Db 781 ATGCCAGAACGGATAACCACTTATGAGATGGACGGGAAAGTCTGTCAAGT 840
 QY 281 PheValLysLysIleAspGlnIthAlaAlaIleAlaAlaIleAlaAlaAspGlnAlaSerLeu 300
 Db 841 TTTGTTAAAAAAATGATCAAACTGCTCACTTAGGTCATSTGGAGATCAAGCGAATTTA 900
 QY 301 ValAlaLeuLeuGluIys 306
 Db 901 GTAGGACTTTAGAAAAA 918

RESULT 3
 US-09-752-069A-30
 / SEQUENCE 30, Application US/09752069A
 / GENERAL INFORMATION:
 / APPLICANT: Dougherty, Thomas J.
 / APPLICANT: Pucci, Michael J.
 / APPLICANT: Dougherty, Brian A.
 / APPLICANT: Davison, Daniel B.
 / APPLICANT: Brucocelli, Robert E.
 / APPLICANT: Thassassi, Jane A.
 / APPLICANT: Farmer II, Bennett T.
 / TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
 / TITLE OF INVENTION: FOR CELL VIABILITY AND THEIR USES
 / FILE REFERENCE: D001INP
 / CURRENT APPLICATION NUMBER: US/09/752,069A
 / CURRENT FILING DATE: 2006-12-29
 / PRIOR APPLICATION NUMBER: 60/174,089
 / PRIOR FILING DATE: 1999-12-30
 / NUMBER OF SEQ ID NOS: 338
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 30
 / LENGTH: 921
 / TYPE: DNA
 / ORGANISM: Streptococcus pneumoniae
 US-09-752-069A-30

Alignment Scores:
 Pred. No : 1. 58s-141 Length: 921
 Score: 1518.00 Matches: 306
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 29 Gaps: 0

US-09-308-397-2 (1-306) × US-09-752-069A-30 (1-921)

QY 1 MethionylSthrlaPheIeuPheIeuGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
 Db 1 ATGACTAAACAGCTTTTATTCCTGGTCAAGGTGCGCAAGTACTGGATGGACGG 60
 QY 21 AspPheTyrAspGlnTyrProIleValLeuAspIleGlnGlyAspIleGlnValLeu 40
 Db 61 GATTCTATGATCATGATTCGATGTTAAGAACGATTGATGGGCAACTGAGCTC 120
 QY 41 GlyTyrAspLeuAspTyrIleLeuAspThrGluIuAspIleLeuAsnGlnThrArgTyr 60
 Db 121 GGTGTTGATTGCGTTATTCATGATTCGATGCGACTCAGGCGCTATGACGCCCTAT 180
 QY 61 ThrgInProAlaIleLeuIaThrSerValAlaIleTyrArgLeuLeuGlnLysGly 80
 Db 181 ACGAAACGACGCCATTAGGACTCTACCTACGGTTGCTATCTACGGTTTGCAAGAAAGGGC 240
 QY 81 ThrgInProAsnMetValAlaGlyIleSerLeuIleGlyIleTyrSerAlaLeuValAlaSer 100

APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
 SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
 FOR DIAGNOSTIC THERAPEUTICS

NUMBER OF SEQUENCE ADDRESSES: 5206
 CORRESPONDENCE ADDRESS: Lynn A Doucette-Stamm and David Bush
 ADDRESSSE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454

COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: <Unknown>
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,433
 FILING DATE: 20-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/ 085131
 FILING DATE: May 1, 1998
 APPLICATION NUMBER: 60/051553
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arniello, Pamela Deneke
 REGISTRATION NUMBER: 40 489
 REFERENCE/DOCKET NUMBER: GTC-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 794:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 924 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETIC: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Streptococcus pneumoniae

FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1..924
 SEQUENCE DESCRIPTION: SEQ ID NO: 794:

US-09-107-433-794

US-09-308-397-2 (1-306) x US-09-107-433-794 (1-924)

Alignment Scores:

Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	
Pred. No.:	4	Score:	151.00	Length:	924	Score:	151.00	Length:	924
Percent Similarity:	100.00%	Matches:	306	Percent Similarity:	100.00%	Conservative:	0	Percent Similarity:	100.00%
Best Local Similarity:	100.00%	Mismatches:	0	Best Local Similarity:	100.00%	Indels:	0	Best Local Similarity:	100.00%
Query Match:	100.00%	Gaps:	0	Query Match:	100.00%	Gaps:	0	Query Match:	100.00%
DB:	15			DB:	15			DB:	15

1 MetThrIlysThrAlaPheIleuPheAlaGlyGlnIleuAlaGlnTrpIleuGlyMetGlyArg 20
 4 ATGACTAAACAGCTTCTTATTGCTGTCAGCTGCCAGPATCTAGGATGGACGG 63
 21 AspPheTyrAspGlnTrpIleuValyGluThrIleAspGlnAlaSerGlnValLeu 40
 64 GATTCCTATGATCAGTATCGATGTTAAAGAACGATGATGAGCAGTCAGGTGTC 123
 41 GlyTyrAspIleuArgTyrLeuIleAspThrGluIleAspLysIleuAspGlnThrArgTyr 60
 124 GGTATGATTGCGTATCTCATGATAGGAAGGCAAACTCAATGAGACCCGCTAT 183
 61 ThrGlnProAlaIleLeuIleSerValAlaThrSerValAlaIleLeuIleArgLeuIleGlnGluIlysIle 80

184 AGCGAACAGCCATTCTGGGACTTCGGTATCTACCGTTATTGCAAGAAAGGGC 243
 81 TyrGlnProAspMetValAlaGlyLeuSerIleGlyGluTyrSerIleLeuValAlaSer 100
 244 TATAGCCCTGATATGGCTGTCTCTCTGAGAAATACTCTGCCTGTGGAAAGC 303
 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
 304 GGCCCTGGATTGAGATCTGGCTAAGGTGAGCTAAGGTGAGCTATGGAA 363
 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
 364 GAACGGCTCTGGTGTCTGGCAATGGTAGACTTCTAAATGCCAGTAGGTC 423
 141 IleGluGluAlaCysGlnLysAlaSerGluIleGlyValValIleValAsnThrProAlaAsnTyrAsn 160
 424 ATTGAGAGGCCCTCAAAAGTTGAACTTGACTGGTAACTCCAGCCAACTATAAC 483
 161 ThrProAlaGlnIleLeuValAlaGlyGluValAlaValAspArgAlaValGluIle 180
 484 ACACCTGCACAAATCGTCAATTGTCATTGTTGGAAAGTGTGGCAGTGTGAGCCGTTGAACTT 543
 161 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHi-sThr 200
 544 TTGGAGAGGAGCAGGTGCCAAAGCTTGATTCTCTAAGGTTCAAGTCCCTTTCACCC 603
 201 AlaIleLeuGluProAlaSerGlnLysIleuAlaGluThrIleLeuAlaGlnValSerPheSer 220
 604 GCTTCCTTGAGCAGTAGCCAAACTGTGAAACTCTAGCTCTAGGTTAGTTTCA 663
 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
 664 GATTTTACGTGTCCTAGTCGCAAACTACAGTGAATACAGAGCTCTGTGATGCAAAAAGGGCATT 723
 241 AlaGlnIleLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
 724 GCTAGGCTCTTGGGCTAGCTTCAAGGAACCGTTCGGTTCTATGAAAGTATTGGGTC 783
 261 MetGlnGluAlaGlyIleSerAspPheIleGlyIleGlyProGlyLysValLeuSerGly 280
 784 ATGGAAAGGAGCAGGCAAAAGCAACTTATCGAGATTCGACGGGAAAGTCTTGTAGGT 843
 281 PheValIleLysIleAspGlnIleAlaHisLeuIleIleValGluAspGlnAlaAspLeu 300
 844 TTTGTTTAAATAATGATCAAATCTAGCTACTGTOACTTAGCTCATGGAAAGTCAGCGAGTTA 903
 301 ValAlaLeuGlyLys 306
 904 GTAGCACTTTAGAAAAA 921

RESULT 6

1-10-158-844-7/C
 Sequence 7, Application US/10158844
 GENERAL INFORMATION:
 APPLICANT: Kunsch et al.
 TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 391
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R
 COMPUTER: Dell Latitude Pentium 3
 OPERATING SYSTEM: Windows 98
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/158-844
 FILING DATE: 03-Jun-2002
 CLASIFICATION: 435/230

Db 721 GCTCAGCTCTGACCGTAGGCAAGCACCGTCTTATGAAAGTATTGGTC 780
 Qy 261 MetGlnGluAlaGlyIleSerAspIleLeuGluIleGlyPrcGlyLysValLeuSerGly 280
 Db 781 ATGCAAGAAGCAGCATAAGCAACTTTCGAGATTGGCCGGAAAGTCtttGAGGT 840
 Qy 281 PheValLysIleAspGlnThrAlaHisLeuAlaIleIvaGluAspGlnAlaSerLeu 300
 Db 841 TTGTTTAAGAAAAATTGATAAAACTGCTTACCTAGCTATGTCAGATGCAAGATTA 900
 RESULT 9
 PCT-US97-22578-43
 Sequence 43, Application PC/TUS9722578
 GENERAL INFORMATION:
 APPLICANT: Baltz, Richard H.
 APPLICANT: Burgett, Bradley S.
 APPLICANT: Dehoff, Stanley G.
 APPLICANT: Jaskunas Jr., Stanley R.
 APPLICANT: Mills, Bradley J.
 APPLICANT: Morris, Franklin H.
 APPLICANT: Peery, Robert B.
 APPLICANT: Rostek, Jr., Paul R.
 APPLICANT: Skarup, Paul L.
 APPLICANT: Smith, Michele C.
 APPLICANT: Rockey, Pamela K.
 APPLICANT: Young-Bellmon, Michele
 TITLE OF INVENTION: Streptococcus pneumoniae DNA Sequences
 NUMBER OF SEQUENCES: 228
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eli Lilly and Company
 STREET: Lilly Corporate Center
 CITY: Indianapolis
 STATE: Indiana
 COUNTRY: U.S.
 ZIP: 46285
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Webster, Thomas D.
 REGISTRATION NUMBER: 39 872
 REFERENCE/DOCKET NUMBER: X-11162
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317-276-3334
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3580 base pairs
 TYPE: Nucleic acid
 STRANDBEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 PCT-US97-22578-43

US-09-308-397-2 (1-306) x PCT-US97-22578-43 (1-3580)
 Qy 1 MetThrLysThrAlaIleIvaGluAlaGlyIleLeuGlyAlaGluGlyIleLeuGlyArg 20
 Db 718 ATGATAAACAGCCTTTTATTGCTGTCAGGCCAGTATCTGGATGGACGG 777
 Qy 21 AspPheTyrAspGlnIleProIleLeuGluThrIleAspArgAlaSerGlnValLeu 40
 Db 778 GATTCTATGATGATTGATGATGAGATGTTAAAGAACGTTAGTCGGTGTAA 837
 Qy 41 GlyTyrAspLeuIgTyrLeuIleAspPheGluGluIleAspLeuAsnGlnThrArgTyr 60
 Db 838 GGTTATGATTGCTTATCTCATGATAAGGAAAGCAGAAACTCAATGAGCCGCTAT 897
 Qy 61 ThrGlnProIleLeuAlaIleIvaGluIleLeuIleLeuGluAlaSerLeu 100
 Db 898 ACGGAAACGCCATTCTAGCAGCTCGGTTGCTATCACCGTTATGCAAGAAAGGGC 957
 Qy 81 TyrGlnProAspPheValAlaGlyIleSerLeuIgIleGlyIleLeuSerIleLeu 100
 Db 958 TATGCCCTGATATGCTGTTGCTGTTGAGATACTCTGCTTGGCAAGGC 1017
 Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaIleIvaAlaIleIvaAlaIleIva 120
 Db 1018 GCGGCTTGGATTTGAGATGGGTCGCTTGCTGCTGCTGCTGCTGCTGAA 1077
 Qy 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValAlaAsnThrProValGluVal 140
 Db 1078 GAAGGGGCGTCGACTGACTCTGGAAAGTGGTCAATACCCAGTAGAGGTC 1137
 Qy 141 IleGluGluAlaCysGlnLysAlaSerGluIleGlyValValThrProAlaAsnTyrAsn 160
 Db 1138 ATTGAGAGCCCTCAAAAGCTCTGACTTGGTGTACTCCGCCAACTATCAC 1197
 Qy 161 ThrProAlaGlnIleValLeuAlaIleIvaGluAlaValAspArgAlaValGluLeu 180
 Db 1198 ACACCTGCACAAATCGTCATTGCTGAGACTGCTGAGTCATGTCAGTTCATGAACTT 1257
 Qy 181 LeuGlnGluAlaGlyAlaIleArgLeuIleProLeuIysValSerGlyProPheHisThr 200
 Db 1258 TTGCAAGAAGCAGTGCACAAACGCTGCAAGCCCTTCACAC 1317
 Qy 201 AlaLeuLeuIleGluProAlaSerGlnLysIleuAlaGluThrLeuAlaValSerPheSer 220
 Db 1318 TCTCCCTGAACTGCTGAGCCGAACATAGCTGAATCTGGCTCAGTAAGTTTCA 1377
 Qy 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaIleValMetGlnLysGluAspIle 240
 Db 1378 GATTTACTGTGCCCCATGTCGECATAACAGAGCTGATGTCAGT 1437
 Qy 241 AlaGlnLeuLeuIleArgGlnValLeuIleGluProValArgPheIysGluSerIleGlyVal 260
 Db 1438 GCTCAGCTCTGAGCTAGGTAAAGAAACCGTTCCTTCTATGAGAAGTTGGGTC 1497
 Qy 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
 Db 1498 ATGGAAAGAACGAGCATAAGCAACTPATCGAGATGTCAGTTGTCAGGT 1557
 Qy 281 PheValLysIleAspGlnIleAlaIleIvaHisLeuAlaIleIvaHisLeuAlaIleIva 300
 Db 1558 TTTGTTAAAAAATTGATCAAGCAAACTGCTCACTAGCTCATGTGGAGATCAAGCGAGTTA 1617
 Qy 301 ValAlaLeuLeuGluLys 306
 Db 1618 GTACACITTAAGAAA 1635

RESULT 10
 PCT-US97-22578-43
 Sequence 9482, Application PC/TUS0203987
 ; GENERAL INFORMATION:
 ; APPLICANT: Eliira Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits

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; /TITLE OF INVENTION: proliferation
; /FILE REFERENCE: ELITRA_02AVCP
; /CURRENT APPLICATION NUMBER: PCT/US02/03987
; /CURRENT FILING DATE: 2002-02-02
; /PRIOR APPLICATION NUMBER: 60/267,636
; /PRIOR FILING DATE: 2001-02-09
; /NUMBER OF SEQ ID NOS: 1581
; /SOFTWARE: FastSEQ for Windows Version 4.0
; /SEQ ID NO: 9482
; /LENGTH: 921
; /TYPE: DNA
; /ORGANISM: Streptococcus pneumoniae
; /FEATURE:
; /NAME/KEY: CDS
; /LOCATION: (1) . . . (921)
; /PCT-US02-03987-9482

Alignment Scores:
Pred. No.: 3.96e-141 Length: 3.96e-141
Score: 1.00e-000 Matche
Percent Similarity: 100.00% Conserv
Best Local Similarity: 99.67% Mismat
Query Match: 99.74% Indels
DB: 1 Gaps: 0

US - 09-308-397-2 (1-306) x PCT-US02-03987-9482
Qy 1 MetThrLysThrAlaPheIeuPheAlaGlyG
Db 1 ATGACTAAACAGCCTTTATTTCTGGCGC
Qy 21 AspPheTyrAspGlnTyrProIleLeuIleGlyG
Db 61 GATTCTATGATCACTATCCGATGTCAAAG
Qy 41 GlyTyrAspLeuArgTyrLeuIleAspPheG
Db 121 GGTATGATTGGTTATCTATGATACCG
Qy 61 ThrGlnProAlaIleLeuAlaThrSerValA
Db 181 ACGCACCGCCATCTAGGACCTCGGTG
Qy 81 TyrGlnProAspPheMetAlaAlaGlyLeuSerI
Db 241 TATCGCCGTATGATGGTCTGGTTGTCCTC
Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaL
Db 301 GGGCCTTGAAATTGAAATGCGTTTGCT
Qy 121 GluAlaAlaProAlaAspSerGlyLysMetV
Db 361 GAAGGGCTCTGTCGACTCTGCAAGATGAGATGG
Qy 141 IleGluGluAlaCysGlnIysAlaSerGluL
Db 421 ATTGAGAACGCTGCAAAAGCTCTGAC
Qy 161 ThrProAlaGlnIleValAlaAlaGlyGlyV
Db 481 ACACCTGCAAACTGTCATTGCTGGAGAG
Qy 181 LeuGlnGluAlaGlyAlaLysArgLeuIleP
Db 541 TGTGAGAACGCGTGGCCAAACGCTGATTC
Qy 201 AlaLeuLeuGluProLeuSerGlnLysLeuA
Db 601 GCTCTCCCTGAACTGCTGGCAGMAACTAG
Qy 221 AspPheThrCysProLeuValGlyAsnThrG

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Db 661 GATTATCTGCCCCTAGTGGCAAATACAGAACCTGCTGATGCAAAAGGACATT 720
Qy 241 AlAGlnLeuLeuThrArgGlnValysGluProValArgPheTyrGluSerIleGlyVal 260
Db 721 GCTAGTCCTGAGGTCAGGTCAAGGAAACCGTTCTGTTCTATGAAAGTATGGGTC 780
Db 261 MetGlnGluAlaGlyTleSerAsnPheIleGluIleGlyProGlyValLeuSerGly 280
Db 781 ATGCAAGAGGAGGCTTAAGAACTTATGAGATTGACGGAAAGTTTGTCAAGGT 840
Qy 281 PheValIysLysIleAspGlnThrAlaHisValGluAspGlnAlaSerLeu 300
Db 841 TTGTTAAAAATTGTCAGACTGGTCACTTGTCAATGAGCTATGGAGATCAAGCAGTTTA 900
Qy 301 ValAlaLeuLeuGlyIys 306
Db 901 GTAGCAGCTTTGAGAAA 918

RESULT 11
US-09-815-242-9482
| Sequence 9482, Application US/09815242
| GENERAL INFORMATION:
| | APPLICANT: Haselbeck, Robert
| | APPLICANT: Ohlsen, Kari L.
| | APPLICANT: Zyskind, Judith W.
| | APPLICANT: Wall, Daniel
| | APPLICANT: Trawick, John D.
| | APPLICANT: Carr, Grant J.
| | APPLICANT: Yamamoto, Robert T.
| | APPLICANT: Xu, H. Howard
| TITLE OF INVENTION: Identification of Essential Genes in
| FILE REFERENCE: ELTRA_011A
| CURRENT APPLICATION NUMBER: US/09/815, 242
| CURRENT FILING DATE: 2001-03-21
| PRIOR APPLICATION NUMBER: 60/191, 078
| PRIOR FILING DATE: 2000-03-21
| PRIOR APPLICATION NUMBER: 60/206, 848
| PRIOR FILING DATE: 2000-05-23
| PRIOR APPLICATION NUMBER: 60/207, 727
| PRIOR FILING DATE: 2000-05-26
| PRIOR APPLICATION NUMBER: 60/242, 578
| PRIOR FILING DATE: 2000-10-23
| PRIOR APPLICATION NUMBER: 60/253, 625
| PRIOR FILING DATE: 2000-11-27
| PRIOR APPLICATION NUMBER: 60/257, 931
| PRIOR FILING DATE: 2000-12-22
| PRIOR APPLICATION NUMBER: 60/269, 308
| NUMBER OF SEQ ID NOS: 14110
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO: 9482
| TYPE: DNA
| ORGANISM: Streptococcus pneumoniae
| FEATURE:
| | NAME/KEY: CDS
| | LOCATION: (1) ... (921)
| US-09-815-242-9482

Alignment Scores:
| Pred. No.: 3.96e-141 Length: 921
| Score: 1514.0.0 Matches: 305
| Percent Similarity: 100.00% Conservative: 1
| Best Local Similarity: 99.67% Mismatches: 0
| Query Match: 99.74% Indels: 0
| DB: 31 Gaps: 0

US-09-308-397-2 (1-306) x US-09-815-242-9482 (1-921)
Qy 1 MetThrLysThrAlaPheIeuPheAlaGlyGinglyAlaGlnTyrLeuGlyMetGlyArg 20

```

BEST AVAILABLE COPY

RESULT 14
 US-60-061-998-494
 ; Sequence 94, Application US/60061998
 ; GENERAL INFORMATION:
 ; APPLICANT: LAGABE, ROBERT E.
 ; APPLICANT: CORLEY, NEIL C.
 ; APPLICANT: RUSSO, FRANK D.
 ; APPLICANT: HANNA, AMY L.
 ; APPLICANT: HEATH, JOE D.
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
 ; TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 797
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INOVITE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOE/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 For Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/60/061,998
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/ AGENT INFORMATION:
 ; NAME: CERONE, MICHAEL C.
 ; REGISTRATION NUMBER: 39,132
 ; REFERENCE/DOCKET NUMBER: PM-0006-2P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 845-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 494:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5963 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: SPN1c499
 ; US-60-061-998-494

Alignment Scores:
 Pred. No.: 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlyTyrIleGlyMetGlyArg 20
 Score: 1.51e-137 Length: 5963
 Percent Similarity: 99.67% Matches: 302
 Best Local Similarity: 99.34% Conservative: 1
 Query Match: 98.02% Mismatches: 0
 DB: 50 Inels: 1
 Gaps: 0

US-09-308-397-2 (1-306) x US-60-061-998-494 (1-5963)

QY 41 GLYTyrapSpleuArgTyrLeuIleAspHrGluuAspLysLeuIaLysGlnGlnThrArgTyr 60
 DB 2919 ATGCTAAACAGCCTTTATTGCTGCTCAGGTGCCAATATCTGGATGGAAAGCG 2978

QY 21 AspPheTyrAspGlnTyrProIleValysGluThrIleAspGalaSerGlnValLeu 40
 DB 2979 GATTCATGATCAGTATCGATGTTAAAGAAACGATGATCGAGGAGTCAGGTCTA 3038

QY 61 ThrGlnProAlaLeuIleLeuIaLysLeuIaLysGlnIleGly 80
 DB 3039 GGTTATGATTGCTTATCATGATAGGAAAGCAAACTCAATGAGCCGCTAT 3098

QY 4099 AGCRAACAGCCATCTGGACTCTGGTATCAGTACCGTATATGCGAAAGGGC 3158

RESULT 15
 US-60-061-998-494
 ; Sequence 94, Application US/60061998
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S. ; APPLICANT: Hinkle, Steven C.
 ; APPLICANT: Slater, Steven C. ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Barry S. ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S. ; APPLICANT: Hinkle, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 3B-1-(52052) A
 ; CURRENT APPLICATION NUMBER: US/60/360,039
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO: 42057
 ; LENGTH: 927
 ; TYPE: DNA ; ORGANISM: Lactococcus lactis
 ; US-60-039-42057

Alignment Scores:
 Pred. No.: 1.53e-94 Length: 927
 Score: 1048.00 Matches: 208
 Percent Similarity: 80.52% Conservative: 40

Best Local Similarity:	67.53%	Mismatches:	58
Query Match:	69.04%	Indels:	2
DB:	80	Gaps:	1
US-09-308-397-2 (1-306) × US-60-360-039-42057 (1-927)			
Qy	1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnGlyTyrLeuGlyMetGlyArg 20		
Db	1 ATGAACTAAACAGCATTTATTCTAGGTCAAAGGCCACAAAGCTTGGATGGCACGT 60		
Qy	21 AspPheTyrAspGlnTyrProIleValGlyGluIleAspArgAlaSerIleValLeu 40		
Db	61 GACTTATAACCAATAATGAAACAGTTAACGACTTAAAGCAACTTGTGAAGCAAGTCAGGTTA 120		
Qy	41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60		
Db	121 GGATGATTTGGAACGCTTGTGATTGATAATGAGAAAGAACTAAATGAAACRAACTAC 180		
Qy	61 ThrglnProIleLeuIleLeuIleSerValAlaThrSerValAlaIleTyrArgLeuGlnGluLysGly 80		
Db	181 ACTAACCTCAATTAAACACCTGTGCTATTAGTTAGCTGTTAGTGAATGGGG 240		
Qy	81 TyrGlnProAspMetValAlaGlyIleSerIleGluTyrSerIleValAlaSer 100		
Db	241 ATTAAACCTGACCTTGTGGCTCTAGTCCTGGAAATATTCTGCTTGTGATCTCA 300		
Qy	101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120		
Db	301 GGAATCATTTGATTGTTCAAGGCTTAAGCTTGTGCTTAACGTCCTAAATATGACA 360		
Qy	121 GluAlaAlaProAlaAspSerGlyLysMetAlaValAlaValLeuAsnThrProAlaGluVal 140		
Db	361 GAAGCTGGCACGACATGGTTCTGGTAATGGTGCCTAATGAAACACGACCCGCTTG 420		
Qy	141 IleGluGluAlaCysAlaSerGluLeu-----GlyValValThrProAlaAsn 158		
Db	421 ATTGAGAATTTGCAAGAACGGCGATTAAACGGCGATTATGGTGCAGGAAAT 480		
Qy	159 TyrAsnThrProAlaGlnIleValLeuAlaGlyGluValValAlaValAspArgAlaVal 178		
Db	481 TATAACAGGCCGAAAAATGGTATGGTGTGAGTTGACGGGTGATATGCTGTT 540		
Qy	179 GluIleLeuGluGluAlaGlyAlaIleProLeuIleProLeuIleValSerGlyProPhe 198		
Db	541 GAGTTCTAAAGAACCGGAGTCTCTAAACCTATTGAAATTAAGTTTCAGACCTTTC 600		
Qy	199 HisThrAlaIleLeuGluProAlaSerGlnAlaIleAlaGluThrLeuAlaGlnValSer 218		
Db	601 CATACTGCCAAATTAAACCGCATCTGAAAAATGCTTGGACCTTGGACCTTGTGATAAATGAT 660		
Qy	219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGlu 238		
Db	661 TTATGACCTTTGAAATTACCATTAATCTCAAATACGAGTGTCTAAAGTAATGAAATATGAT 720		
Qy	239 AspIleAlaGlnIleLeuThrArgGlnValAlaProValArgPheTyrGluSerIle 258		
Db	721 GAAGTAAAGGACTTTGACGGTCAAGTCAGTGTGTTTATGAACTCGTT 780		
Qy	259 GlyValMetGlnGluIaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeu 278		
Db	781 GAAACATGCAAAACTAGGGCGACTCGCTGTTTATAAAGTGGTCCTGGGAGAGTACT 840		
Qy	279 SerGlyPheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAla 298		
Db	841 TCAGGGTTCAATTAAAAATTGATAAAAATGCAAAATGCTAATGTGAAATATTAGCT 900		
Qy	299 SerLeuValAlaLeuIleGluLys 306		
Db	901 TCAATTGAAAGCTTTGATTAATGAG 924		

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OM protein - nucleic search, using frame_pplus_p2n model

Run on: June 11, 2003, 20:37:43 ; Search time 660 Seconds (without alignments)

3077.862 Million cell updates/sec

Title: US-09-308-397-2

Perfect score: 1518

Sequence: 1 MTRKAFLFAGQGAQYLGMGR.....QTAHLAHVEDQASLYALLBK 306

Scoring table: BLOSUM62

Xgapop 10.0 / Xgapext 0.5

Ygapop 10.0 / Ygapext 0.5

Fgapop 6.0 / Fgapext 7.0

Dgap 6.0 / Dext 7.0

Searched: 7602234 seqs, 3319262570 residues

Total number of hits satisfying chosen parameters: 15204468

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Command line parameters:

```

-MODEL=frame+p2n.model -DEV=xlp
-Q=/sgn2_6/podata/1/pna/pct_new comb.seq:*
-D=Pending_Patents_NA_New_QMFT=FastB -SUPFIX=_TPN -MINMATCH=0.1 -LCOPOL=0
-LOC_PEXT=0 -BITS=8 -START=1 -END=1 -MATRIX=_global2 -TRANS=_human40_di
-LIST=45 -DOCAUT=PCT -THR SCORE=0.5 -MAXLEN=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFORMAT=PTO -NORMEXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09-0839@CGN_1.1_638 -GRUNAT 06062003_112350_28959 -NCPU=6 -ICPU=3
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREBLOCK=100 -LONGLOG
-NO_NPA -LARGEQUERY -NEG SCORE=0.5 -WAIT -DEBLOCK=100 -XGAPEXT=0.5 -FGAPPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7

```

RESULT 1

US-10-282-122A-37621

; Sequence 37621, Application US/10282122A

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELTRA_034A

; CURRENT FILING DATE: US/10/282,122A

; PRIOR APPLICATION NUMBER: 50/191,078

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1515	99.8	921	9	US-10-282-122A-37621	Sequence 37621, A
2	1108	73.0	918	9	US-10-282-122A-36004	Sequence 36004, A
3	1048	69.0	927	8	US-10-269-193-41057	Sequence 41057, A
4	1036	68.2	919	9	US-10-282-122A-3855	Sequence 3855, A
5	952	62.7	915	9	US-10-282-122A-21491	Sequence 21491, A
6	948	62.5	987	8	US-10-217-884-3319	Sequence 3319, A
7	937	61.7	927	9	US-10-282-122A-20712	Sequence 20712, A

Query Match: 72.99% Indels: 0
 DB: Gaps: 0

US-09-308-397-2 (1-306) × US-10-268-122A-36004 (1-918)

Qy 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlySerGlyArg 20
 Db 1 ATGACAAAACAGCTTATTGCTGGCAAGAGCTAAACATGATGGCAGTT 60

Qy 21 AspPheTyrAspGlnTyrProLeuAlaGlyGlnGlyAlaGlnTyrLeuGlySerGinValLeu 40
 Db 61 GATTGCTATGAAATTACCGATTGCTCAAGAGACTTAAACCGCTATTCAATTG 120

Qy 41 GlyTyrAspLeuAspTyrLeuAspTyrGluAspLysLeuAsnGlnThrArgTYR 60
 Db 121 GGATATGATCTGCGCTTGATTGATTATAATGATGAGAAAGCTTA 180

Qy 61 ThrGlnProAlaLeuAlaThrSerValAlaLeuAlaGlyLeuSerLeuGlyGlnGly 80
 Db 181 GCACAGCCAGGATTTAACCTCGTATTGCTTTGAAAGAAAGCT 240

Alignment Scores:
 Pred. No.: 7.12e-97 Length: 927
 Score: 1048.00 Matches: 208
 Percent Similarity: 80.52% Conservative: 40
 Best Local Similarity: 67.53% Mismatches: 58
 Query Match: 69.04% Indexes: 2
 DB: 8 Gaps: 1

US-09-308-397-2 (1-306) × US-10-369-493-42057 (1-927)

Qy 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
 Db 1 ATGACTAAACGCAATTATTCTCGGCTTACGGGCACAAAAGTTGGATGGACGT 60

Qy 21 AspPheTyrAspGlnTyrProLeuAlaGlyGlnGlyAlaGlnTyrLeuGlySerGlnValLeu 40
 Db 61 GACTTATGACCAATATGAAACAGTTAAAGCAACTTTGATGAACTGCAAGCTTA 120

Qy 41 GlyTyrAspLeuArgTyrLeuLeuAspPheGluGlyAspLeuGlyGlnGly 60
 Db 121 GGATATGATTGCGGCTTGATTGATAATGATGAGAAAACACTAAATGAAACAGTAC 180

Qy 61 ThrGlnProAlaLeuAlaThrSerValAlaLeuAlaGlyLeuSerLeuGlyGlnGly 80
 Db 181 ACTCACTGGCAATTAAACACCTGTTACGTTGCTTACGTTGGTTAACGATGGG 240

Qy 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValAlaGlyLeuSerAlaSerGly 20
 Db 361 ACAGCACCACCCGCTGAGTGGGGAAAATGCTGCTGTAACTG 420

Qy 141 IleGluGluAlaCysGlnLysAlaSerGlnLeuGlyValValAlaProAlaGlyTyr 160
 Db 421 ATTGAGAGATTGGTCAAGAACGCTTAAAGCCGCTTAAGCCGCTTAAATTATA 480

Qy 161 ThrProAlaGlnIleValAlaAlaGlyGluValAlaValAspArgAlaValGluLeu 180
 Db 481 ACTCTCACACAAATGTTATGTTATGGTGGAACTGAGTAGCTGGTGGAACT 540

Qy 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProProHisThr 200
 Db 541 TAAAGGGAGCTGGTGTAAACGTTCTCTAAAGTTCTGTCCTTOATAG 600

Qy 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGlnValSerPheSer 220
 Db 601 GCTCTTGGAAATCTGTGTTAAATGCTCAAGTTGAAATTATAAGCTGAAGGAGATT 660

Qy 221 AspPheThrCysProLeuValGlyAlaGlyGlnValAlaValMetGlnLysGluAspIle 240
 Db 661 GATTTCATGCTTCACTAGTGGGAACATCAAGCTGAATTATAAGCTGAAGGAGATT 720

Qy 241 AlaGlnLeuLeuGluAlaGlyTyrLeuGlySerGlnLeuAlaGlnValSerGly 280
 Db 781 ATGCAAAATTTGGTGTGAACTACTGCAATTGCAAGTGGCTGCTTCTGCTGTA 780

Qy 261 MetGlnGluAlaGlyTyrLeuGlySerAsnPhenIleGluGlyProGlyLysValSerGly 280
 Db 840 MetGlnGluAlaGlyTyrLeuGlySerGlnLeuAlaGlnValSerGly 840

Qy 281 PheValValGlyAspGluThrAlaIleIleGlyGluAspGlnAlaSerLeu 300
 Db 841 TTTGAAAGATGATGAAATCTGCAAAAGTCAGCTGTGAAGACTTAGCTAGTTG 900

Qy 301 ValAlaLeuGlu 305
 Db 901 CAGGCTTCTTAGAT 915

RESULT 3
 US-10-369-493-42057 Application US/10369493
 ; GENERAL INFORMATION

Qy 179 GluLeuLeuGlnGluAlaGlyAlaValSerLeuLeuAlaSerGlyLeuAlaSerGly 198
 Db 541 GAGTGCTAAACGCGGAGTTGCAACTATGAATAAGTTTCAAGGACTCTTC 600

Qy 199 HisThrAlaLeuLeuGluProAlaSerGlnLysLeuAlaGluGlyLeuAlaSerGly 218
 Db 601 CATACTGAAATTAAACGAGATCTGAAATGAGCTTGGAGCTTGGTGTGAT 660

Qy 219 PheserAspPheThrCysProLeuValGlyAsnThrGluAlaAlaAlaAlaAlaMetGlnLysGlu 238
 Qy 661 TTAGACCTTGTAAATTACATTAACTCTAAATCGAGTGTAAAGTAATGGAAATGAT 720
 Db 239 AspPheAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerile 258
 Db 721 GAACTAAAGGACTTTGAGGGTAAGCATGGAAACAGTGTGTTTATGAACTGGT 780
 Qy 259 GlyValMetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeu 278
 Db 781 GAAACATGCAAAACTAGGGCCACTCGCTTATGAACTGGAGTGTGCTGGAGACTT 840
 Qy 279 SerGlyPheValLysLysIleAspGlnThrAlaLisLeuAlaHisValGluAspGlnAla 298
 Db 841 TCAGGTTTCATAAAAAAATGATAAAAATGCAAAAATGCAAAATGCTAAATGTTGAAATTTAGCT 900
 Qy 299 SerLeuValAlaLeuLeuGluLys 306
 Db 901 TCTATGAAAGCTTGTGATTAATCAG 924

RESULT 4
 US-10-282-122A-38525
 ; Sequence 38525, Application US/10282122A
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cherry
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlisen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; FILE REFERENCE: EIJTRA 034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SEQ ID NO: 38525
 ; LENGTH: 939
 ; SOFTWARE: PatentIn version 3.1
 ; TYPE: DNA
 ; ORGANISM: Streptococcus pyogenes
 US-10-282-122A-38525

Alignment Scores:
 Pred. No.: 1.21e-95
 Score: 1036.00
 Database: Similarity: 0.95
 Length: 939
 Matches: 209
 Concentration: 29

Best Local Similarity	68.30%	Mismatches:	58
Query Match:	68.25%	Indels:	0
DB:	9	Gaps:	0
US-09-308-397-2 (1-306) × US-10-282-122A-38525 (1-939)			
Qy	1 MethionylthiophosphateLeuPheAlaGlyGlnGlyAlaGlnT		
Db	1 ATGACAAAGACGCCCTTTTARTGGGTCAAGGTTCTCAAA		
Qy	21 AspPheThrAspAlanylProlevalleuGluThrIleAspA		
Db	61 GATTTTATGAACTTGGCTGATTTGTAAGAAAACCTTGTGAC		
Qy	41 GlyTyrosPheLeuArgTyLeuIleAspThrGluGluAspLysL		
Db	121 GATAACGATTGGCCGTTGATGATGAGTGCAGTTAAAC		
Qy	61 ThreonineProAlaIleLeuAlaThrSerValAlaIleTyArgL		
Db	181 ACCGAAACCAGCTATTGACATGATCAATTGCTATTACCGTGTG		
Qy	81 TyrGlnProAspMetValAlaIgLyLeuSerLeuGluGluTyRS		
Db	241 GTTAAACCGGATTCGGCTGGCTCTTCTCTAGGAGAAATCT		
Qy	101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysA		
Db	301 GGCGCACTCTCTTTGAGATAACCTATCCTAGTAGCTTAAAGA		
Qy	121 GluAlaAlaProAlaAspSerGlyMetValAlaLeuLeuA		
Db	361 GAGCGAGCAACAAAGGATCTGGAAAATGGTTGCCCTTAAGA		
Qy	141 IleGluGluAlaLysGinLysAlaSerGluLeuGlyValValT		
Db	421 ATCGAAGAGTCGTGTCATATAGGGCTPAACATGGAGTGGTGC		
Qy	161 ThrProAlaGlnIleValleuAlaGlyGluValValAlaValA		
Db	481 ACTCTCTGAAATTGAAATTGGTGGTCAGACAGATGTTGTA		
Qy	181 LeuGluGluAlaGlyAlaLysArgLeuIleProLeuIleValS		
Db	541 TTAAAGGAAGGGAGGTTAAAGCTTTAACCCCTTAACCGTT		
Qy	201 AlaLeuLeuGluProAlaSerGinLysLeuAlaGluThrLeuA		
Db	601 GCTTGGTAGAACAGTAGCCCTTGTGGTAAAGTGGTAAAGTGG		
Qy	221 ASPPheThrCysProLeuValGlyAsnThrGluAlaAlaValM		
Db	661 GACTCTCAAGATCTTGTGTTGTTGTTGTTGTTGTTGTT		
Qy	241 AlaGlnLeuIleThrGlnValAlaSerGluProValArgPheT		
Db	721 CCAGAACATTAGCCCGTCAAAGTCATGGAGCTGTTGTTGTT		
Qy	261 MetGlnGluAlaGlyIleSerAnPheIleGluIleGlyPro		
Db	781 TTCTAGAAGTGGCTACACATTGTTGACTGTTGAGTGGACCAAG		
Qy	281 PheValLysLysLeuAspCinThrAlaHisLeuAlaHisValC		
Db	841 TTGTGAGAAATGATAAAAATTACTATGTTACTAGTGTGTT		
Qy	301 ValAlaLeuLeuGluIys 306		
Db	901 CGTTTATTGTTGATGAGA 918		

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hausebeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Yamamoto, Robert
 APPLICANT: Carr, Grant
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITIA 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/205,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/220,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: Patent In version 3.1

SEQ ID NO: 21491

LENGTH: 21491

TYPE: DNA

ORGANISM: Enterococcus faecium

US-10-282-122A-21491

Alignment Scores:

Pre. No.: 4.19e-87

Length: 915

Score: 952.00

Matches: 189

Percent Similarity: 78.36%

Best Local Similarity: 61.97%

Query Match: 62.71%

DB: 9

Gaps: 2

RESULT 6

US-10-282-122A-21491 (1-915)

Qy 3 LysThrAlaPheLeuPheAlaLysGlnArgLysGlnArgLysGlnAspPhe 22

Db 4 ARNACGCGTCCTTATTGCGCAAGGCGCAGATTCAGGATGCGGCTAC 120

Qy 23 TyrAspGlnTyrProLeuLeuGlyLysGlnLeuGlyLysGlnLeuGlyTyr 42

Db 64 TATGAAAGA---GCCGTGTAAAGCAGACATTGAAAGTGGGATCATC 240

Qy 43 AspLeuArgTyrLeuLeuAspThrGluGluAspLysLeuAspGlnThrArgTyrThrGln 62

Db 121 GATATGGCTGAACTTCTTCAGAAATAACGTTGATCAGCGCTATAACAG 180

Qy 63 ProAlaAlaLeuAlaThrSerValAlaLeuTyrArgLeuLeuGlyLysGlyTyrGln 82

Db 181 CCAGCTTATCTAACGTGAGTCGCTTATPCTGCTTATGAAAGGAGCATTC 240

Qy 83 ProAspMetValAlaGlyLeuSerIgGlyGluTyrSerAlaLeuValAlaSerGlyAla 102

GENERAL INFORMATION:

APPLICANT: LeuAspPheGluAspAlaValAlaLeuAlaLysArgGlyAlaTyrMetGluGluAla 122

Db 301 CTATCCCTACTGAACTGCTAGTGGCTTATGACAGAGCT 360

Qy 123 AlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProAlaGluValLeuGlu 142

Db 361 GGCCTACTGAAAGCCGAAATGGTGCAGTGAAGATGCGCTTGTGACGTCAGTCAG 420

Qy 143 GluAlaCysGlnLysAlaSerGluLeuGlyValValAlaLeuAsnThrPro 162

Db 421 GAAAGCTGTCTGAACCTAGAAAGTGGGATCTGATCCTCTGAAATTATAACCT 480

Qy 163 AlaGlnLeuValAlaGlyGluValValAlaValAlaAspArgAlaValGluLeuGln 182

Db 481 CAGCAGATCGTCATGGGGAAAGCAGTAACGAAAGCTGAAAT 540

Qy 183 GluAlaGlyAlaLysArgLeuLeuProLeuLysValSerGlyProPheHisThrAlaLeu 202

Db 541 GAAAAGGTCTCAAAGAATGATGCTCTAAATGTCAGGCCCTTCATACAGTATT 600

Db 542 LeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSerAspPhe 222

Db 601 TAGAACCGGAGCAAAACACTGGGAAGGACCTTAAGTCAGATTCATCTCTGACCT 660

Qy 223 ThrCysProLeuValGlyAlaSerGlnLysGluAlaLavalMetGlnLysGluAspIleAlaGln 242

Db 661 TCTTTCTCTATAAGCAACAAACGAAATAATGAGAAAGAACATCGGGGA 720

Qy 243 LeuLeuThrArgGlnValLysGluProValArgPheTyroGlyLeuGlyValMetGln 262

Db 721 CTACTGACAGAACTGCAACCTGTTCTATGAGATTCATAAGTAAAGTAAA 780

Qy 263 GluAlaGlyIleSerAsnPheIleGlyLysGluLeuSerGlyPheVal 282

Db 781 ACAATCGGCATCGAACAACTGATGAGTCGCCCCGAAAGTATAAGGGATTATG 840

Qy 283 LysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnLysLeu----- 300

Db 841 AAAAAATCGATAAAATAACGTTCTGCTGTTGAGATAAGGAGACATTGGTGA 900

Qy 301 --ValAlaLeuLeu 304

Db 901 ACAATGCAATACTA 915

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

US-10-417-884-3319
 Sequence 319, Application US/10/417884

ADDRESS: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02454

GENERAL INFORMATION:

APPLICANT: Lynn A. Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

COMPUTER READABLE FORM:

COMPUTER: PC

MEDIUM TYPE: CD-ROM ISO9660

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/417,884

FILING DATE: 17-APR-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: JULY 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Aminieio, Pamela Denise
 REGISTRATION NUMBER: 40,489
 REGISTRATION/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 893-5007
 TELEFAX: (781) 893-8277
 INFORMATION FOR SEQ ID NO: 3319:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 987 base pairs
 TYPE: nucleic acid
 STRANDBNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1.. 987
 SEQUENCE DESCRIPTION: SEQ ID NO: 3319:
 US-10-417-884-3319

Alignment Scores:
 Pred. No.: 1..18e-86 Length: 987
 Score: 948.00 Matches: 188
 Percent Similarity: 78.03% Conservative: 50
 Best Local Similarity: 61.44% Inmatches: 63
 Query Match: 62.45% Inmatches: 4
 DB: 8 Gaps: 2

US-09-308-397-2 (1-306) x US-10-417-884-3319 (1-987)

QY 3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyLeuGlyMetGlyArgAspPhe 22
 DB 73 AAAACAGGATCTTATTAGTGGCCAAGGTGCAAAATCANGTAAAGGAAAGATTAA 132
 QY 23 TyrAspGlyTyrProIleValysGluThrIleAspArgAlaSerGlnValLeuGlyTyr 42
 DB 133 TATGAGAA--GCCGTGTAAACGAGACATTGTGAAGCAAGTCTGGCTAC 189

QY 43 AspLeuArgTyrLeuIleAspTyrGluGlyAspLysAsnLysThrArgTyrGln 62
 DB 190 GATAGGCTGAACTTGCTTACAGAAATGAGCTTGTGATAGACCAATAACAG 249

QY 63 ProAlaLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGlyLysGlyTyrGln 82
 DB 250 CCAGGTATTAAAGTCGATGCGTATTATGCTTGTGAGGAGCATGAATATC 309

QY 83 ProAspMetValAlaIleGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSerGlyAla 102
 DB 310 CCAGATGCACTTGTAGCTGAGCTTGTAGCTGTTAGAGATATTGGCTATTAGTGTAGTGC 369

QY 103 LeuAspPheGluAlaValAlaLeuAlaIleGlyAspGlyAlaTyrMetGluGluAla 122
 DB 370 CTATGCTTCTACTGAGCACTGCTTGTAGCTGAGCTTGTAGCTTGTAGCT 429

QY 123 AlaProAlaAspSerGlyLysMetValAlaValLeuAlaThrProValGluValIleGlu 142
 DB 430 ACCCGAACGCTGCGAACGGGAAGCGGAAAGCTTGCTAGTGTAGTGTGCGATGCG 489

QY 143 GluAlaCysGlnLysAlaSerGluLeuGlyValThrProAlaAsnTyrAsnThrPro 162
 DB 490 GAAACGTGATGAGCTGCAAGTACGCCATCTATCCCTGCAAATTATAACCT 549

QY 163 AlaGlnIleValIleAlaGlyGluValAlaValAspAlaValGluLeuLeuGln 182
 DB 550 CAGGAGATCGTGTGTCGCGAAGAAAGCAGTAGCGAAAGCTGTTACTATAAA 609

QY 183 GluAlaGlyAlaLysArgLeuIleProLeuIleProLeuIleSerGlyProPheHisThrAlaLeu 202
 DB 610 GAAAAGCCCTCAAAAGATGATCCCTCTAAATGTCAGGGCCCTTTCATACGCTATT 669

QY 203 LeuGluProAlaSerGlnLysLeuAlaIleGluThrLeuAlaGlnValSerPheSerAspPhe 222
 DB 670 TTGAAACGGCACAAAAAACTGGCAAGGACCTTGTAGTCAGATTCATTCTGAACT 729

QY 223 ThreysProLeuValGlyAsnThrGlnAlaAlaAlaMetGlnGlyGluAspIleAlaGln 242
 DB 730 TCTTTCTCTATCATAGAAACAAACACGGAAATAATGAAAGAAACATCGCCGA 789

QY 243 LeuIeuthArgGlnValIleGlyGluProValArgPheTyrGluSerIleGlyValMetGln 262
 DB 790 CTATTCGACAGGAGTGTGATGCACTCTGCTTGTATGAGATGAGTCAATAGTTAAA 849

QY 263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
 DB 850 ACAATGGATTCATGAACTGAACTGATGAACTGCTGCTGTTGAACTAAGCTTAAGCGGATTTATG 909

QY 283 LysysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu---- 300

DB 910 AAAAAATGATAAAACATACGAGTCTGCTGTTGAACTAAGCTTAAGCGGATTTATG 969

QY 301 --ValAlaLeu 304
 DB 970 ACAATGGCTATACTA 984

RESULTS 7
 US-10-282-122A-20712
 Sequence 20712, Application US/10282122A
 / GENERAL INFORMATION:
 / APPLICANT: Wang, Liangsu
 / APPLICANT: Zamudio, Carlos
 / APPLICANT: Malone, Cheryl
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Ohlsen, Kari
 / APPLICANT: Zyskind, Judith
 / APPLICANT: Wall, Daniel
 / APPLICANT: Trawick, John
 / APPLICANT: Carr, Grant
 / APPLICANT: Yamamoto, Robert
 / APPLICANT: Foreyth, R.
 / APPLICANT: XU, H.
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 / FILE REFERENCE: ELITRA-03A
 / CURRENT APPLICATION NUMBER: US/10/282,122A
 / CURRENT FILING DATE: 2003-02-20
 / PRIOR APPLICATION NUMBER: 60/191,078
 / PRIOR FILING DATE: 2000-03-21
 / PRIOR APPLICATION NUMBER: 60/206,848
 / PRIOR FILING DATE: 2000-05-23
 / PRIOR APPLICATION NUMBER: 60/207,727
 / PRIOR FILING DATE: 2000-10-23
 / PRIOR APPLICATION NUMBER: 60/230,335
 / PRIOR FILING DATE: 2000-09-06
 / PRIOR APPLICATION NUMBER: 60/230,347
 / PRIOR FILING DATE: 2000-09-09
 / PRIOR APPLICATION NUMBER: 60/242,578
 / PRIOR FILING DATE: 2000-10-23
 / PRIOR APPLICATION NUMBER: 60/253,625
 / PRIOR FILING DATE: 2000-11-27
 / PRIOR APPLICATION NUMBER: 60/257,931
 / PRIOR FILING DATE: 2000-12-22
 / PRIOR APPLICATION NUMBER: 60/267,636
 / PRIOR FILING DATE: 2001-01-09
 / PRIOR APPLICATION NUMBER: 60/269,308
 / PRIOR FILING DATE: 2001-02-16
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 78614
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 20712

LENGTH: 927
 TYPE: DNA
 ORGANISM: Enterococcus faecalis
 US-10-282-122A:20712

Alignment Scores:
 Pred. No.: 1.44e-85 Length: 927
 Score: 937.00 Matches: 187
 Percent Similarity: 51.17% Conservative: 40
 Best Local Similarity: 61.92% Mismatches: 75
 Query Match: 61.73% Indels: 0
 DB: 9 DB: 904 ACGTAA 909

RESULT 8
 US-09-134-000C-1582
 Sequence 1582, Application US/09134000C
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 PRIORITY APPLICATION NUMBER: US 60/7055,778
 PRIORITY FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1582
 LENGTH: 948

TYPE: DNA
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-1582

Alignment Scores:
 Pred. No.: 1.48e-85 Length: 948
 Score: 937.00 Matches: 187
 Percent Similarity: 75.17% Conservative: 40
 Best Local Similarity: 61.92% Mismatches: 75
 Query Match: 61.73% Indels: 0
 DB: 6 DB: 6

US-09-134-000C-1582 (1-927)
 Qy 3 LysThrAlaPheLeuPheLeuAlaGlyGlnGlyAlaGlnTyLeuGlyMetGlyArgAspPhe 22
 Db 4 AAAACAGGATTTATTAGTCGACAGGGCCCAAGTATAAGGATGGTGAGAAATTAA 63

Qy 23 TyrAspGlnTrpProLeuValLysGluThrTleLeuPArgAlaSerGlnValLeuGlyTy 42
 Db 44 TATCACCAGAACGGATTGTTGGGAAACCTTCGATGAAACAGCATCTTAAAGTT 123

Qy 43 AspLeuArgTrpLeuLeuAspThrGluGluAspLysLeuAsnGlnThrArgTrpThrGln 62
 Db 124 GAGATGCCAGAACTTGTCTTACTGAAAGCTTTAAATGAAACGTTAAATGAA 183

Qy 63 ProAlaLeuLeuAlaThrSerValAlaLeuLeuAlaLeuLeuGlnGluLysGlyTyGln 82
 Db 184 CCTGCTATTAACTTCAGTCGATTACCGCTCTTGCAACAAAGGCTACG 243

Qy 83 ProAspMetValAlaGlyLysLeuSerLeuGlyLysLysLeuSerAlaLeuValAlaSerGlyAla 102
 Db 244 CCTGATCGTGCGGTTTAACTGCTCTTGCAAGGGGGCT 303

US-09-1308-397-2 (1-306) × US-09-134-000C-1582 (1-148)
 Qy 3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyLeuGlyMetGlyArgAspPhe 22
 Db 22 AAAACAGGATTTATTAGTCGACAGGGCCCAAGTATAAGGATGGTGAGAAATTAA 81

Qy 123 AlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluValIleGlu 142
 Db 364 GCAACACAAGGAACTGCAAAATGCTGCTGTTGTTGAACTGCGCTTAACTGCGCTTGG 423

Qy 143 GluAlaGlySglNlysAlaSerLysLeuGlyAlaValThrProAlaAsnTrpAsnThrPro 162
 Db 424 AAAGCTTCCAAAGGCAAGCAGCTTCCTGAAATTGCTCAGCAATTATAAACACCA 483

Qy 163 AlaGlnTrpLeuLeuAlaGlyGluValAlaValAspArgAlaValGluLeuGln 182
 Db 484 CRACAATCGTGTATTGCTGGTGGTTAGGTGCTGCTGATGACCTCTCAA 543

Qy 183 GluAlaGlyAlaLysArgLeuLeuProLeuLysValSerGlyProPheHisThrAlaLeu 202
 Db 544 GAGCTGTGGTAAAGCAATTGTCCTTAATGTCGTTAGTCGCTTCAACGGCTG 603

Qy 203 LeuGluProAlaSerGlyLysLeuAlaGlyLeuLeuAlaGlySerProSerAspPhe 222
 Db 604 TTACAACGGCATCAAATGGCTCAGGATTGCAAAATTGAACTTCAAACGATG 663

Qy 223 ThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIleAlaGln 242
 Db 664 CAAATTCTGTCAATTGCAATTGCACTGCGCAATTGCGCAATTCAAGGGCG 723

Qy 243 LeuLeuThrArgGlnValLysGluProValArgPheGlyLysLeuValMetGln 262
 Db 724 TATTCGAAARGCAAGTCATGCTGGGTTACGTTGAAAGCAGATCGAAACGATGAAAG 783

Qy 263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValSerGlyPheVal 282
 Db 784 GCTATGAAGTAAACGATGTTGAAGTGTCTCCGGAAACATTAACCTGTTTT 843

Qy 283 LysLysIleAspGlnThrAlaLysLeuAlaHisValGluAspGlnAlaSerLeuValAla 302

Db 904 ACGTAA 304

Qy 163 GluAlaGlyAlaLysArgLeuLeuProLeuLysValSerGlyProPheHisThrAlaLeu 202

Percent Similarity: 75.17% Conservative: 40 Sequence 15949, Application US/10282122A
 Best Local Similarity: 61.92% Mismatches: 75 ; GENERAL INFORMATION:
 Query Match: 61.73% Indels: 0 ; APPLICANT: Wang, Liangshu
 DB: 8 Gaps: 0 ; APPLICANT: Zanudio, Carlos
 US-09-308-397-2 (1-306) x US-10-434-665-1582 (1-948) ; APPLICANT: Malone, Cherry
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Olsen, Kari
 ; APPLICANT: Zykind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Truwick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,336
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 15949
 ; LENGTH: 927
 ; TYPE: DNA
 ; ORGANISM: Clostridium acetobutylicum
 ; US-10-282,122A-15949

Alignment Scores:
 Pred. No.: 1.69-62 Length: 927
 Score: 710.50 Matches: 146
 Percent Similarity: 67.11% Conservative: 56
 Best Local Similarity: 48.80% Mismatches: 96
 Query Match: 46.81% Indels: 3
 DB: 9 Gaps: 3

US-09-308-397-2 (1-306) x US-10-282-122A-15949 (1-927)

Qy 3 LysThrAlaPheLeuPheAlaGlyGlyGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe 22
 Db 622 TTACACCGCATTAAGAAATTGGCTAGGATTACAAATTGAACTTCAAACGATGAG 681
 Qy 23 TyrAspGlnTyrProIleValGlyProIleGlyAsnThrAlaLeu 202 ;
 Db 562 GAACTCGTGTGAAAGGATGATGTTCCGCTTCAACGGCTG 621
 Qy 203 LeuGluProAlaSerGlnIleValAspLeuIleGlyAlaGlnValSerPheAspPhe 222
 Db 622 TTATGGAAAGGCAAGTCATGTTGCGCTTCAAGAGAACGATGAG 801
 Qy 263 GluAlaGlyIleSerAspPheIleGlyGlyProIleGlyAsnThrAlaLeu 282
 Db 802 GCTATGAACTGGTAGAACGATGATGAACTTGGTCCAGGAAACATTAACGTGTTGTT 861
 Qy 283 LysLysIleAspGlnThrAlaHisLeuAlaHisLeuAlaSerLeuValAla 302
 Db 862 AAAAATGACAAACATTGAAATGGCAACATTTGCAAGATGTTGAACTTACAGTGTGCTT 921
 Qy 303 LeuLeu 304
 Db 922 ACCTTA 927
 RESULT 11
 US-10-282-122A-15949

127 AAAACAGCAGAAATTGCTGAAAGGAAAGATGAACTGAACT 186
 62 GlnProAlaIleLeuAlaIleSerValAlaIleLeu---GlnGluLysGly 80
 187 CAGCCAGCAGCTTAAATTACTAGTATAGTGTGCTTAAAGGAACTTGAAGGAA 246

US-10-282-122A-41191
 Sequence 41191, Application US/10282122A
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forstch, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELTRA-034A
 CURRENT APPLICATION NUMBER: US/10/282,1122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-11
 PTO: PRIOR APPLICATION NUMBER: 60/205,848
 PRIOR FILING DATE: 2000-05-23
 PTO: PRIOR APPLICATION NUMBER: 60/207,727
 PTO: PRIOR APPLICATION NUMBER: 60/230,335
 PTO: PRIOR FILING DATE: 2000-09-16
 PTO: PRIOR APPLICATION NUMBER: 60/230,347
 PTO: PRIOR FILING DATE: 2000-09-09
 PTO: PRIOR APPLICATION NUMBER: 60/242,578
 PTO: PRIOR FILING DATE: 2000-10-23
 PTO: PRIOR APPLICATION NUMBER: 60/253,625
 PTO: PRIOR FILING DATE: 2000-11-27
 PTO: PRIOR APPLICATION NUMBER: 60/257,931
 PTO: PRIOR FILING DATE: 2000-12-22
 PTO: PRIOR APPLICATION NUMBER: 60/267,636
 PTO: PRIOR FILING DATE: 2001-02-09
 PTO: PRIOR APPLICATION NUMBER: 60/269,308
 PTO: PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or P.M.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 41191
 LENGTH: 939
 TYPE: DNA
 ORGANISM: *Vibrio cholerae*
 US-10-282-122A-41191

Alignment Scores:
 Pred. No.: 4.29e-57 Length: 939
 Score: 657.50 Matches: 146
 Percent Similarity: 66.23% Conservative: 58
 Best Local Similarity: 47.40% Mismatches: 97
 Query Match: 43.31% DeB: 7
 Gaps: 9

US-09-308-397-2 (1-309) x US-10-282-122A-41191 (1-939)

Qy 1 MetThrLysThrAlaPheLeuIleSerAlaGlyIleGlnGlnIleLeuGlyMetClyArg 20
 Db 16 ATGAGTAAGTGTGCTATGTATTCCGGTCAGGGCTCGCAGCATGAGTGTGGCT 75

Qy 21 AspPheTyrAspGlnTyrProIleValyGluThrIleAspArgAlaSerGlnValLeu 40
 Db 76 GACCTTGGCGAAGATGAAATTAACATTGGCGAAAGCTAGAACTGCTT 135

Qy 41 GlyTyrAspLeuArgTyrLeuLeuAspLysLeuAsnGlnThrArg 59
 Db 136 GGTTACGATCTGTGGCCCTGGTCAAGATGCCCTGTGAGAATCTAACAAACTTC 195

Qy 60 TyrThrGlnProAlaLeuIleSerValAlaIleTyrArgLeuGlnGlnLys 79
 Db 196 CGTACTAACCTGGTCTTCCGCCCTGTGCAATGGCAGAACTRG 255

Qy 80 GlyTyr---GinProAspMetValAlaGlyLeuSerIleGlyGluItySerAlaLeuVal 98
 Db 256 GCTCTAGCAACCTGGTCTTGTGTTAGTGTGTCAGGTGCTGATATTGCGACTGTA 315
 Qy 99 AlaSerGlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaItyr 118
 Db 316 TGTGCGGCGGATGATGTTAAACAGGATCAACCTGGTGAAGTGGTGGTGTGATTG 375
 Qy 119 MetGluGluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProVal 138
 Db 376 ATGCAACAGGCGCTGCCGTGCGGTACGGTGAATTAACGCAATCGGCTAGAGAT 435
 Qy 139 GluValIleGluGluAlaCysGlnLysAlaSerGluIleGlyValWaltwProAlaAsn 158
 Db 436 GAGGCAATGTTAAAGCTGCTGCGGCGCAGGTGAAAGTGCCTCCCTGTAAC 495
 Qy 159 TyrAspThrProAlaGlnIleValAlaGlyGluValValAlaValAspArgAlaVal 178
 Db 496 TTAACTCACCAGGCCAGTGGTATGGTGTGTCAGTAAAGATGCGGTGCGGGC 555
 Qy 179 GluLeuGlnGlnGluAlaGlyAlaLysLeuAlaGluThrIleSerGlnValLeu 198
 Db 556 GTCCTGTTAAGAAGGGGCCGAAGCTGGCTGAGTGGCTGCTCTGCCAGTTCCTGAC 615
 Qy 199 HisThrAlaIleLeuGluProAlaSerGlnLysLeuAlaGluThrIleSerGlnValSer 218
 Db 616 CACTGGCTTGTGATGAACTCCCTGGGATGATTGCAAAACCTAGCAGAGCTGAA 675
 Qy 219 PheSerAspPheThrCysProLeuValGlyAsnAlaAlaValMetGlnLysGlu 238
 Db 676 TTCAATGACCACAAATTCCGGTCATCAAATACGTTGAT-----GTTGTCGCTGAAACG 729
 Qy 239 Asp-----IleAlaGlnLeuIleThrArgGlnValLysGluProValArgPheTyr 255
 Db 730 GATCCGGTAATTAATTAAGATGGTGTGATTCCTCAACTCTAGGCCAGTCGTTGACT 789
 Qy 256 GluSerIleGlyValMetGlnGluAlaGlyIleSerAsnPhenylGluIleGlyProGly 275
 Db 790 GATGCGTTGAAACAAATAGGCCACAAAGTGTGCAAAAGCTGATGAAATGGGCCGGT 849
 Qy 276 LysValLeuSerGlyPheValIysLysLeuAspGlnThrAlaHisLeuAlaHisValGlu 295
 Db 850 AAGTATGACTGCTTAACAAACGTTATTGTAACAAACCTAGAAAGGTGTGCGCAGTCAT 909
 Qy 296 AspGlnAlaSerIleLeuValAlaLeu 303
 Db 910 GACCTGGCTTCCTGGATGCGCTG 933

RESULT 14
 US-10-359-493-41012
 ; Sequence 41012, Application US/10369493
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; Hinkle, Gregory J.
 ; Slater, Steven C.
 ; Goldman, Barry S.
 ; APPLICANT: Chen, Xiantang
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 3B-10 (54052) B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO: 41012
 ; LENGTH: 942
 ; TYPE: DNA
 ; ORGANISM: *Bacillus halodurans*
 ; Alignment Scores:
 US-10-359-493-41012

Alignment Scores:

Pred. No.:	9.78e-57	Length:	942
Score:	654.00	Matches:	141
Percent Similarity:	64.40%	Conservative:	58
Best Local Similarity:	45.63%	Mismatches:	106
Query Match:	43.08%	Indels:	4
DB:	8	Gaps:	4
US-03-308-397-2 (1-306) × US-10-369-493-41012 (1-342)			
Qy 1 MetThrLysThrAlaPheLeuPheAlaGlyLysGlnGlnGlnGlnGlnGlyMetGlyArg 20			
Db 1 ATGGCAAAATGTAGCATTCATTCAGGCTAACGTCAGCTTCAGGATGGCAGGCAGGC 60			
Qy 21 AspPheTyrAspGlnTyrProLleValLysGluThrLlePheGlnGlnGlnValLeu 40			
Db 61 GAATTACTTCAGGGAAAAA---GCAAAAGGATTTTGAGGCCGGATGAAACACTC 117			
Qy 41 GLYTYAspLeu---ArgTyrLeuIleAspPheGluGluAspLysLeuAspGlnTrpArg 59			
Db 118 GGCTATCCCTTCAAGCATATGTTGAGGGCCGAGAAATTGCGCGGGGGAA 177			
Qy 60 TyrIleGlnProAlaLeuIleAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLys 79			
Db 178 AATACGCCAACGGGCTTGTGACGATGAGCAGCAGCAGCGGTTTATCGTCGCGGTAAATAT 237			
Qy 80 GLYTYGlnProAspMetValAlaGlyLeuSerLysGluGluTyrSerAlaLeuValAla 99			
Db 238 GGAATTAACCTGTATATAAGCCGGTCATGTCAGTGTGGGTACAGTGTGGCT 297			
Qy 100 SerGlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLeuAspGlyAlaTrpMet 119			
Db 298 TCAAGGCTCTAACGTTGCGATGGCTGTGACGGTTCATACCGGGTGTGGTTGTTATG 357			
Qy 120 GluGluAlaAlaProAlaAspSerGlyLysIleSerValAlaValLeuAsnThrProValGlu 139			
Db 358 GAAAGACGGTACCATTCGGCGAAGGAGCAATGGCTCCATCTGGCATGGGCCGAC 417			
Qy 140 ValIleGluGluAlaGlyGlnLysAlaSerGluLeuGly---ValIleValProAlaAsn 158			
Db 418 GAATTGAAACAGTAACTGAAAGCAGGCTAACAGAGCAGGCCGGCTGTCCTTGAACTTGCCAAAC 477			
Qy 159 TyrAsnThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaVal 178			
Db 478 TTAAACTGTCTGGGAAATATGTCATCTCAGTTCTGCTGGGCTTCGAAAGGATCA 537			
Qy 179 GluLeuIeGlnGluAlaGlyAlaIleAspGluIleIleProLeuIleSerGlyProPro 198			
Db 538 GAGGAACCAAGGAAACAGGGCAAGGGCGGAAAGCCGATGTCATGAACTGAGCGGACCGTT 597			
Qy 199 HisThrAlaIleLeuGluProAlaAspSerGlnLysLeuAlaGluIleGluLeuAlaGlnValSer 218			
Db 598 CATTACGCTATGAAACCGCTGGCGAAAGCTGATGTCATGAACTGAGCTGTTAGCGGATTTGGCA 657			
Qy 219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnIys--- 237			
Db 658 ATCGCTATGGCGTCAACCTTTATGCCCATGTCAGAGATTCGTTCAAAAGCC 717			
Qy 238 GluAspIleAlaGlnIleLeuThrArgGlnValLysGluProValArgPheTyglUser 257			
Db 718 GCTGAATTCGCTCATCTCATTTGCAAGCTACTCTCAGTTCGTTGGCAGGCACT 777			
Qy 258 IleGlyValMetGluGluAlaGlyIleSerAspNHsPheIleGluIleGlyProGlyIysVal 277			
Db 778 GTTCGTCGCACTCTCTGAGCTGGAGCTGATGCTGGAAATCGGATTCGGAATGTTG 837			
Qy 278 LeuSerGlyPhenylalanylSlysIleAspGlnThrAlaHisLeuAlaIleIleSerGln 297			
Db 938 CTCTCAAGGCCCTGTCCTCCCAACTACGCGCTAACGTTAATGTTTCTGAGTCATCGG 897			
Qy 298 AlaSerIleValAlaLeuLeuGluLys 306			
Db 898 GCAAGGATTTGAGGATGGTAAAGAAA 924			

RESULT 15
 US-10-282-122A-32186
 Sequence 32186 Application US/10282122A
 GENERAL INFORMATION:
 / APPLICANT: Wang, Liangu
 / APPLICANT: Zamudio, Carlos
 / APPLICANT: Malone, Cheryl
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Ohlsen, Kari
 / APPLICANT: Zyskind, Judith
 / APPLICANT: Wall, Daniel
 / APPLICANT: Trawick, John
 / APPLICANT: Carr, Grant
 / APPLICANT: Yamamoto, Robert
 / APPLICANT: Forsyth, R.
 / APPLICANT: Xu, H.
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 / FILE REFERENCE: ELTRA-034A
 / CURRENT APPLICATION NUMBER: US-10-282-122A
 / CURRENT FILING DATE: 2003-02-20
 / PRIOR APPLICATION NUMBER: 60/194,078
 / PRIOR FILING DATE: 2000-03-21
 / PRIOR APPLICATION NUMBER: 60/206,848
 / PRIOR FILING DATE: 2000-05-23
 / PRIOR APPLICATION NUMBER: 60/207,727
 / PRIOR FILING DATE: 2000-05-26
 / PRIOR APPLICATION NUMBER: 60/230,335
 / PRIOR FILING DATE: 2000-09-06
 / PRIOR APPLICATION NUMBER: 60/230,347
 / PRIOR FILING DATE: 2000-09-09
 / PRIOR APPLICATION NUMBER: 60/242,578
 / PRIOR FILING DATE: 2000-10-23
 / PRIOR APPLICATION NUMBER: 60/253,625
 / PRIOR FILING DATE: 2000-11-27
 / PRIOR APPLICATION NUMBER: 60/257,931
 / PRIOR FILING DATE: 2000-12-22
 / PRIOR APPLICATION NUMBER: 60/267,636
 / PRIOR FILING DATE: 2001-02-09
 / PRIOR APPLICATION NUMBER: 60/269,308
 / PRIOR FILING DATE: 2001-02-16
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 32186
 / LENGTH: 930
 / TYPE: DNA
 / ORGANISM: *Proteus mirabilis*
 US-10-282-122A-32186

Alignment Scores:
 Pred. No.: 2.76e-56
 Score: 649.50
 Percent Similarity: 63.84%
 Best Local Similarity: 47.23%
 Query Match: 40.79%
 DB: 9
 DB: 3
 DB: 3

US-09-308-397-2 (1-306) x US-10-282-122A-32186 (1-930)

Qy 1 MetThrLysThrAlaPheLeuIleGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg
 Db 1 AGACTGATTGCGATGGTTCCGAAAGGATCAAGGCAATTGATGTTGCA

Qy 21 AspPhetyrAspGlnIyrProleVallySgluThrIleAspArgAlaserGlnValLeu
 Db 61 GAACTGCGGAGCAATTGACAGAAATTTGCTCAAGCATGATGATTTG
 Qy 41 GlyTyrAspIleArgTyrLeuIleAspThr--GluGluAspLysLeuGlnGlnThrArg
 Db 121 GGTATTCCTGCGATTGTCGAAATGCTGAAGAGTTAAACAAACATGG
 Qy 60 TyrThrGlnPnroAilLeuAlaIhrSerValAlaIleGlyLeuIglnGlnLys

Db 181 AAAACACCCGGCATATTAGCAGCATCCGTCATTGGCGAGTATGGCAAGAAAA 240
 QY 80 ---GlyTyrGlnProAspMetValAlaGlyLeuSerLeuGlyGlutYrSerAlaLeuVal 98
 Db 241 CAAGGAAATGGCACAAATGATGAGTCAGTCAGCTCAAGTCTGGAGATTCCTTATGTC 300
 QY 99 AlaSerGlyAlaLeuAspPheGluAsp2AlaValAlaLeuValAlaLysArgGlyAlaTyr 118
 Db 301 TGTCCTGGTAATTGATTTGCTGCCGATTAACTAGTACAATGGCGGTCAATTAA 360
 QY 119 MetGluGluAlaAlaProlAlaAspSerGlyLysMetValAlaValLeuAspThrProVal 138
 Db 361 ATGCAAGGGCTTACCTGAGCTACGGCCATGTGCAATTATGGGATTAGATAAT 420
 QY 139 GluValIleGluGluAlaLysGlySerGlyLeuGlyValThrProAlaAsn 158
 Db 421 GAGCTATGGCAAAGCTGTGAGAATGGGCTCAAGGACAAGTTGTCACCTGAGAC 480
 QY 159 TyrAsnThrProAlaGlnIleValIleAlaGlyGluValAlaValAspArgAlaVal 178
 Db 481 TTACTACCCGTCATGGTATCGGTATAAAGAACCGTAGGGTGAAGGG 540
 QY 179 GluIleLeuGlnGluAlaGlyAlaLysGlyLeuIleProLeuIleSerGlyProPhe 198
 Db 541 GCATTATGAAAGCTGAGCAAGCTGCTTACCTTGCGGTTACCTTGCGGTAAGTGCCCTCT 600
 QY 199 HisThrAlaLeuLeuGluProAlaSerLysLeuAlaGluThrLeuAlaGlnValSer 218
 Db 601 CACTGTGCTTAATGAAAGCTGCTGCATAAGTTGGTGTGCAATTGCAAGAAATGAA 660
 QY 219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAla--AlaValMetGlnLys 237
 Db 661 TTAAACACCTGAAATCAAATGTTAAATGTTGAAAGCAAAACCGATGCT 720
 QY 238 GluAspPheAlaGlnLeuLeuThrArgGlnValGlyProValAlaGlyPheTyrGluSer 257
 Db 721 AATGCTATTCGAGATGCAATTAGTCGTCAGCTTATAAACCCAGTCCCTGGACTGAAAG 780
 QY 258 IleGlyValMetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysVal 277
 Db 781 GTTGAATTTATGCTGGTGGAGGATCAACATTTAGATAAGCTACCCGTAATGTA 840
 QY 278 LeuSerGlyPheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGln 297
 Db 841 TTAACGTTAAAGAAACCTTCAAAAGAGATGAACGTCAGCAGTTAATGATAATT 900
 QY 298 AlaSerIleValAlaLeu 304
 Db 901 GCATCATTTAGACGCTGCATTA 921

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